



PT		useful for suppressing tumor growth
XX		
PS	Claim 4; Page 82-83; 99pp; English.	
CC		
CC	A novel method of inhibiting endothelial cell growth comprises	
CC	contacting the cells with calreticulin (or its fragments/variants).	
CC	Fragments of calreticulin causes at least 40% inhibition of angiogenesis,	
CC	tumor growth and/or endothelial cell growth (claimed). The method may be	
CC	used for inhibiting angiogenesis in a patient. The angiogenesis is	
CC	associated with a disease other than a tumor that is associated with	
CC	neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,	
CC	trachoma, neovascular glaucoma, psoriasis, angiodermas, immune	
CC	inflammation, atherosclerosis, excessive wound repair, retinal	
CC	neovascularization, macular degeneration, corneal graft rejection,	
CC	contact lens overwear, Crohn's disease, non-immune inflammation,	
CC	rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,	
CC	Goumert's syndrome, systemic vasculitis, scleroderma, Sjogren's	
CC	sndrome, sarcoidosis and primary biliary cirrhosis). The method may	
CC	also be used for treating/inhibiting tumor growth especially	
CC	Kaposi's sarcoma (claimed).	
XX		
SQ	Sequence 49 AA:	
	Query March 100.0%; Score 49; DB 21; Length 49;	
	Best Local Similarity 100.0%; Pred. NO. 4.6e-48;	
	Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
QY	1 NYKGNVLINRKDEFTHLTYLIVRPDNTYEKKIDNSGVESGSL 49	
Dd	1 NYKGNVLINRKDEFTHLTYLIVRPDNTYEKKIDNSGVESGSL 49	
	RESULT 2	
ID	AAV92354 standard; Protein; 60 AA.	
AC	AAV92354:	
DT	10-AUG-2000 (first entry)	
XX		
DE	Recombinant human calreticulin residues 121-180.	
XX		
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;	
KM	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;	
KW	Cytosolic; dermalogical; immunosuppressive; anti-inflammatory; hepatic;	
XX	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PX	WO200020577-A1.	
XX		
PD	13-Apr-2000.	
XX		
PF	05-OCT-1999; 99WO-US3240.	
XX		
PR	06-OCT-1998; 98US-0103438.	
XX		
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	
PI	Tosato G, Pike SE, Yao L;	
DR	WPI; 2000-303767/26.	
XX		
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin,	
PT	useful for suppressing tumor growth	
XX		
PS	Claim 4; Page 85; 99pp; English.	
CC		
CC	A novel method of inhibiting endothelial cell growth comprises	
CC	contacting the cells with calreticulin (or its fragments/variants).	
CC	Fragments of calreticulin causes at least 40% inhibition of angiogenesis,	
CC	tumor growth and/or endothelial cell growth (claimed). The method may be	

CC	used for inhibiting angiogenesis in a patient.
CC	The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g., diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The method may also be used for treating/inhibiting tumor growth especially Kaposi's sarcoma (claimed).
XX	
SQ	Sequence      60 AA:
Query Match	100.0%; Score 49; DB 21; Length 60;
Best Local Similarity	100.0%; Pred. No. 5.6e-48;
Matches     49;	Conservative    0; Mismatches    0; Indels        0; Gaps            0;
DY	1 NYKGNVLINRKDEFTHLVTLIVRPDNTYEKKIDNSGVESGSL E 49 
Db	12 NYKGNVLINRKDRCKDEFTHLVTLIVRPDNTYEKKIDNSGVESGSLE 60 
RESULT 3	
ID	AAY92352
XX	AAY92352 standard; Protein: 61 AA.
AC	
XX	AAY92352;
DT	10-AUG-2000 (first entry)
XX	
DE	Recombinant human calreticulin residues 120-180.
XX	
KW	MBP-calreticuliclin; maltose binding protein; angiogenesis; inhibition; endothelial cell; anti-angiogenic; neuroprotective; antidiabetic; cytosolic; dermatologic; immunosuppressive; antinflammatory; hepatic; anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
KM	
KX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FN	WO2000020577-A1.
PN	
PD	13-APR-2000.
PE	05-OCT-1999; 99WO-US23240.
PR	06-OCT-1998; 98US-0103438.
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI	Tosato G, Pike SE, Yao L;
DR	WPI: 2000-303767/26.
XX	
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin, useful for suppressing tumor growth
PS	Claim 4; Page 82-83; 99pp; English.
XX	
CC	A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants).
CC	Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g., diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

XX Sequence 61 AA;

Query Match 100.0%; Score 49; DB 21; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5,7e-48;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGKNNVLINRKDKDEFTLHYTLVPRDNTYEKKIDNSQVSGSLE 49  
DB 13 NYGKNNVLINRKDKDEFTLHYTLVPRDNTYEKKIDNSQVSGSLE 61  
|||||

RESULT 4  
ID AAY92351 standard; Protein: 180 AA.

AC AAY92351;

DT 10-AUG-2000 (first entry)

DE Human vasostatin (calreticulin N-terminal 180 amino acids).

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;  
KW angiotensin; inhibition; endothelial cell; anti-angiogenic;  
KW neuroprotective; antidiabetic; cytosolic; dermatological; hepatic;  
KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;  
KW gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.  
OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth

PS Claim 4; Page 82; 99pp; English.

CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants)  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

XX Sequence 180 AA;

Query Match 100.0%; Score 49; DB 21; Length 180;  
Best Local Similarity 100.0%; Pred. No. 1.6e-47;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGKNNVLINRKDKDEFTLHYTLVPRDNTYEKKIDNSQVSGSLE 49  
DB 132 NYGKNNVLINRKDKDEFTLHYTLVPRDNTYEKKIDNSQVSGSLE 180  
|||||

RESULT 5  
ID AAY92355 standard; Protein: 280 AA.

AC AAY92355;

DT 10-AUG-2000 (first entry)

DE Recombinant delta-120 calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytosolic; dermatological; immunosuppressive; anti-inflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.  
OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth

PS Claim 4; Page 86; 99pp; English.

CC This sequence comprises recombinant human calreticulin (AAY92350)  
CC missing the N-terminal 120 amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The  
CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

XX Sequence 280 AA;

Query Match 100.0%; Score 49; DB 21; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGKNNVLINRKDKDEFTLHYTLVPRDNTYEKKIDNSQVSGSLE 49  
|||||

DB 12 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSQVESGSL 60

RESULT 6  
AAV92350  
ID AAV92350 standard; Protein; 400 AA.  
XX  
AC AAV92350;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant human MBP-calreticulin.  
XX  
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cystic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US23240.  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Tosato G, Pike SE, Yao L;  
XX  
DR WPI: 2000-303767/26.  
DR N-PSDB; AAA09346, AAA09347.  
XX  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
PS Claim 4; Page 80-81; 99pp; English.  
XX  
CC Recombinant human MBP-calreticulin comprises the sequence of human  
CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The  
CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 400 AA:

Query Match 100.0%; Score 49; DB 21; Length 400;  
Best Local Similarity 100.0%; Pred. No. 3.4e-47;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSQVESGSL 49  
|||||  
DB 132 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSQVESGSL 180

RESULT 7  
AAW11156  
ID AAW11156 standard; peptide; 401 AA.

XX  
AC AAW11156;  
XX  
DT 31-MAY-1997 (first entry)  
XX  
DE Calreticulin.  
XX  
KW calreticulin; C-domain; restenosis; inhibitor.  
XX  
OS Homo sapiens.  
XX  
PN WO9636643-A1.  
XX  
PD 21-NOV-1996.  
XX  
PF 17-MAY-1996; 96WO-1B00471.  
XX  
PR 16-MAY-1996; 96US-0649417.  
XX  
PR 17-MAY-1995; 95US-0442844.  
XX  
PA (UYAL-) UNIV ALBERTA.  
XX  
PI Lucas A, Michalak M;  
XX  
DR WPI: 1997-012036/01.  
XX  
XX  
PT Inhibition of restenosis in patients - using calreticulin or a  
PT C-domain polypeptide of calreticulin or a variant with the same  
PT activity.  
XX  
PS Disclosure: Fig 1; 48pp; English.  
XX  
CC The present sequence is calreticulin. It and a C-domain derived peptide  
CC (AAW06736) are useful for treating a patient to inhibit restenosis. The  
CC calreticulin-type cpds. are administered either parenterally,  
CC intravenously or via a catheter and can target areas of vascular damage  
CC to inhibit or prevent restenosis.  
XX  
SQ Sequence 401 AA:

Query Match 100.0%; Score 49; DB 18; Length 401;  
Best Local Similarity 100.0%; Pred. No. 3.4e-47;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSQVESGSL 49  
|||||  
DB 132 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSQVESGSL 180

RESULT 8  
AAP92276  
ID AAP92276 standard; protein; 417 AA.  
XX  
AC AAP92276;  
XX  
DT 23-FEB-1990 (first entry)  
XX  
DE 60 kD Ro (Ro/SSA) antigen.  
XX  
KW Sjorens syndrome; systemic lupus erythematosus.  
XX  
OS Synthetic.  
XX  
PN WO8909273-A.  
XX  
PD 05-OCT-1989.  
XX  
PF 22-MAR-1989; 89WO-US01213.  
XX  
PR 22-MAR-1988; 88US-0171634.  
XX  
PA (TEXA ) UNIV OF TEXAS SYST.



PI Sontheimer RD, Capra JD, McCauliffe DP;  
 XX WPI: 1989-309537/42.  
 DR N-PSDB; AAP92276.  
 XX  
 XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen  
 PT - used in immunoassays to detect rheumatic disease  
 XX  
 PS Disclosure; Fig 2; 88pp; English.  
 CC  
 CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
 CC expressed recombinantly to detect autoantibodies, for identification  
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,  
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
 CC antigens.  
 CC  
 XX  
 SQ Sequence 417 AA;  
 Query Match 100.0%; Score 49; DB 10; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-47;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NYKGNVLINRCKDDEFTLTYLIVRPDNTYEVKIDNSQVESGSLE 49  
 DB 149 NYKGNVLINRCKDDEFTLTYLIVRPDNTYEVKIDNSQVESGSLE 197  
 ||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 9  
 AAY00927  
 ID AAY00927 standard; Protein: 417 AA.  
 XX  
 AC AAY00927;  
 XX  
 DT 28-MAY-1999 (first entry)  
 XX  
 DE Calreticulin.  
 XX  
 KW C1q and collectin receptor; C1qR binding domain; complement ubiquitin;  
 KW CUB functional; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9907406-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 12-AUG-1998; 98WO-GB02430.  
 XX  
 PR 12-AUG-1997; 97GB-0016998.  
 XX  
 PA (UYLE-) UNIV LEICESTER.  
 XX  
 PI Schwaebel W;  
 XX  
 DR WPI: 1999-180404/15.  
 XX  
 PT Use of a C1qR binding domain - to modulate complement ubiquitin  
 PT (CUB) functionality.  
 XX  
 PS Disclosure; Page 26-27; 31pp; English.  
 XX  
 CC This sequence is calreticulin, a homologue of C1q and collectin receptor  
 CC (C1qR). The invention relates to the use of a C1qR binding domain in a  
 CC medicament to effect complement ubiquitin (CUB) functionality, and an  
 CC inhibitor of the C1qR binding domain in a medicament to inhibit CUB  
 CC functionality. The C1qR binding domain, or its inhibitor, can be used to  
 CC treat a human or animal body. Particularly an inhibitor is used to treat  
 CC complement activation involved in the initiation and maintenance of  
 CC inflammation, for example in myocardial infarction, brain ischaemia  
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus

CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
 CC plaques in Alzheimer's disease. The use of C1qR binding domain or  
 CC inhibitor enables the CUB domain functionality to be modulated using a  
 CC low molecular weight molecule.  
 CC  
 XX  
 SQ Sequence 417 AA;  
 Query Match 100.0%; Score 49; DB 20; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-47;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NYKGNVLINRCKDDEFTLTYLIVRPDNTYEVKIDNSQVESGSLE 49  
 DB 149 NYKGNVLINRCKDDEFTLTYLIVRPDNTYEVKIDNSQVESGSLE 197  
 ||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 10  
 AAY92349  
 ID AAY92349 standard; Protein: 417 AA.  
 XX  
 AC AAY92349;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Human MBP-calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; anti-diabetic;  
 KW cytosolic; dermatologic; immunosuppressive; anti-inflammation; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..17  
 FT /label= signal\_peptide  
 FT Protein 18  
 FT /label= mature\_protein  
 XX  
 PN WO200020577-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI: 2000-303767/26.  
 DR N-PSDB; AAA09346, AAA09347.  
 XX  
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX  
 PS Disclosure; Page 79-80; 99pp; English.  
 XX  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants)  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

SQ Sequence 417 AA;

Query Match 100.0%; Score 49; DB 21; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.5e-47;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 49  
DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197

RESULT 11

ID AAE24591 standard; Protein; 417 AA.

AC AAE24591;

DT 04-OCT-2002 (first entry)

DE Human calreticulin protein.

KM Human; calreticulin; antisense compound; hyperproliferative disorder;  
KM cancer; autoimmune disease; viral infection; cardiovascular disease;  
KM antisense therapy; cytostatic; immunosuppressive; virucide.

OS Homo sapiens.

PN WO200236743-A2.

PD 10-MAY-2002.

PF 30-OCT-2001; 2001WO-US49045.

PR 30-OCT-2000; 2000US-0702327.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowseert LM;

DR WPI: 2002-479759/51.

DR N-PSDB; AAD39469.

PT Novel antisense compound targeted to nucleic acid encoding

PT calreticulin, useful for treating a human having disease or condition  
PT associated with calreticulin e.g. cancer, viral infection, autoimmune  
PT disease -

PS Disclosure; Page 88-90; 109pp; English.

CC The invention relates to antisense compounds, compositions and methods  
CC for modulating the expression of calreticulin. The compositions comprise  
CC antisense compounds, particularly antisense oligonucleotides, targeted  
CC to nucleic acids encoding calreticulin. The antisense compound is useful  
CC for inhibiting the expression of calreticulin in human cells or tissues.  
CC It is also useful for treating a human having a disease or condition  
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.  
CC cancer, autoimmune disease, viral infection or cardiovascular disease,  
CC by inhibiting expression of calreticulin. It is useful for diagnostics,  
CC therapeutics, prophylaxis and as research reagents and kits. It is also  
CC used in antisense therapy. The present sequence is human calreticulin  
CC protein. This sequence is used in the exemplification of the invention.

SQ Sequence 417 AA;

Query Match 100.0%; Score 49; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.5e-47;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 49  
DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197

DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197

RESULT 12

ID AAU77712 standard; Protein; 417 AA.

AC AAU77712;

DT 05-JUN-2002 (first entry)

DE Human calreticulin (CRT).

KM Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;  
KM cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;  
KM enhanced antigen-specific immune response; cytotoxic T lymphocyte;  
KM tumour; cancer; cervical cancer.

OS Homo sapiens.

PN WO200212281-A2.

PD 14-FEB-2002.

PF 02-AUG-2001; 2001WO-US24134.

PR 03-AUG-2000; 2000US-222902P.

PA (UYJO ) UNIV JOHNS HOPKINS.

PI Wu T, Hung C;

DR WPI: 2002-257463/30.

DR N-PSDB; ABK11662.

PT New nucleic acids encoding a fusion polypeptide comprising an  
PT endoplasmic reticulum chaperone polypeptide linked to an antigenic  
PT polypeptide, useful as a vaccine for inducing antigen-specific immune  
PT responses -

PS Disclosure; Page 27; 71pp; English.

CC The invention describes a nucleic acid molecule (1) encoding a fusion  
CC polypeptide comprising a first polypeptide domain comprising an  
CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and  
CC a second polypeptide domain comprising at least one antigenic peptide  
CC e.g. human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as  
CC a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune  
CC responses, particularly those mediated by cytotoxic T lymphocytes. The  
CC nucleic acid and compositions comprising the nucleic acid is also useful  
CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.  
CC This is the amino acid sequence of the human calreticulin (CRT), an  
CC endoplasmic reticulum protein used in the creation of a DNA vaccine.

SQ Sequence 417 AA;

Query Match 100.0%; Score 49; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.5e-47;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 49  
DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197

RESULT 13

ID AAE18851 standard; Protein; 417 AA.

AC AAE18851;

DT 17-MAY-2002 (first entry)

```
DE Human calreticulin protein.
XX
XX Human: prostate cancer; calreticulin; TR1D-1 protein; TR1ATS protein;
XX androgen action pathway; cell proliferation; kidney cancer; lymphoma;
XX epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
XX cytosolic; U19 protein.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 98..170
XX /label= N-terminal_domain
XX Region 98..103
XX /label= Alpha_helix
XX Region 149..154
XX /label= Alpha_helix
XX Domain 171..285
XX /note= "Proline-rich domain (P domain)"
XX Domain 286..397
XX /label= C-terminal_domain
XX
XX WO200206327-A2.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-US22357.
XX
XX 17-JUL-2000; 2000US-218761P.
XX 16-JUL-2001; 2001US-0906393.
XX
XX (NOUN ) UNIV NORTHWESTERN.
XX
XX Wang Z, Xiao W;
XX WPI: 2002-179780/23.
XX DR N-PSDB: AAD29931.
XX
XX Identifying a subject that is likely to have aggressive form of
XX prostate cancer, involves comparing calreticulin levels in prostate
XX specimen of the subject and in benign prostatic epithelial cells of the
XX same subject.
XX
XX Disclosure: Page 146-148; 148pp; English.
XX
XX The present invention relates to methods of distinguishing aggressive
XX forms of prostate cancer from non-aggressive forms. The method involves
XX comparing the level of calreticulin in prostate specimen and in benign
XX prostatic epithelial cells of a subject. The invention particularly
XX relates to two proteins, namely calreticulin and TR1D-1 (TR1ATS; U19)
XX that are down-regulated in aggressive forms of prostate cancer but not
XX in slowly progressing prostate cancer. They play important roles in
XX the part of androgen action pathway that suppresses cell proliferation
XX and/or prevents prostate cancer. The method is useful for identifying
XX a subject who is likely to have an aggressive form of prostate cancer.
XX The invention further relates to a method of identifying a subject with
XX a slow growing form of prostate cancer. TR1D-1 sequences are useful for
XX treating cancers such as epithelium-derived carcinomas, kidney cancers,
XX lymphomas, leukaemias and prostate cancers. Sequences of the invention
XX are used as vaccines and in gene therapy. The present sequence is human
XX calreticulin protein.
XX
XX Sequence 417 AA:
XX
XX Query Match 100.0%; Score 49; DB 23; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-47;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
AAV00924
XX ID AAV00924 standard; Protein; 122 AA.
XX
XX AAV00924;
XX
XX 28-MAY-1999 (first entry)
XX
XX Human cClqR binding domain protein sequence.
XX
XX C1q and collectin receptor; cClqR binding domain; complement ubiquitin;
XX CUB functionality; inhibitor; complement activation; inflammation;
XX myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
XX rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
XX immune complex nephritis; therapy.
XX
XX Homo sapiens.
XX
XX WO9907406-A1.
XX
XX 18-FEB-1999.
XX
XX 12-AUG-1998; 98WO-GB02430.
XX
XX 12-AUG-1997; 97GB-0016998.
XX
XX (UNL-E-) UNIV LEICESTER.
XX
XX Schwaebler W;
XX WPI: 1999-180404/15.
XX DR N-PSDB: AAX27251.
XX
XX Use of a cClqR binding domain - to modulate complement ubiquitin
XX (CUB) functionality.
XX
XX Claim 9; Page 23; 31pp; English.
XX
XX This sequence is a C1q and collectin receptor (cClqR) binding
XX domain. The invention relates to the use of a cClqR binding domain in a
XX medicament to effect complement ubiquitin (CUB) functionality, and an
XX inhibitor of the cClqR binding domain in a medicament to inhibit CUB
XX functionality. The cClqR binding domain, or its inhibitor, can be used to
XX treat a human or animal body. Particularly an inhibitor is used to treat
XX complement activation involved in the initiation and maintenance of
XX inflammation, for example in myocardial infarction, brain ischaemia
XX (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
XX erythematosus, burns, immune complex nephritis, and to treat amyloid
XX plaques in Alzheimer's disease. The use of cClqR binding domain or
XX inhibitor enables the CUB domain functionality to be modulated using a
XX low molecular weight molecule.
XX
XX Sequence 122 AA:
XX
XX Query Match 73.5%; Score 36; DB 20; Length 122;
XX Best Local Similarity 100.0%; Pred. No. 6e-33;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 15

```
AAV00926
XX ID AAV00926 standard; Protein; 122 AA.
XX
XX AAV00926;
XX
XX 28-MAY-1999 (first entry)
XX
XX Rat cClqR binding domain protein sequence.
XX
XX C1q and collectin receptor; cClqR binding domain; complement ubiquitin;
```

KW CUB functionality; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.

OS Rattus norvegicus.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI: 1999-180404/15.

XX N-PSDB: AAX27253.

PT Use of a cC1qR binding domain - to modulate complement ubiquitin  
 (CUB) functionality.

PS Claim 9; Page 24-25; 31pp; English.

CC This sequence is a C1q and collectin receptor (cC1qR) binding  
 CC domain. The invention relates to the use of a cC1qR binding domain in a  
 CC medicament to effect complement ubiquitin (CUB) functionality, and an  
 CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB  
 CC functionality. The cC1qR binding domain, or its inhibitor, can be used to  
 CC treat a human or animal body. Particularly an inhibitor is used to treat  
 CC complement activation involved in the initiation and maintenance of  
 CC inflammation, for example in myocardial infarction, brain ischaemia  
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
 CC plaques in Alzheimer's disease. The use of cC1qR binding domain or  
 CC inhibitor enables the CUB domain functionality to be modulated using a  
 CC low molecular weight molecule.

XX Sequence 122 AA;

Query Match 73.5%; Score 36; DB 20; Length 122;

Best Local Similarity 100.0%; Pred. No. 6e-33;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 RCKDDEFTHLTYLRPDNTYEKIDNSQVESGSL 49  
 |||

Db 1 RCKDDEFTHLTYLRPDNTYEKIDNSQVESGSL 36

Search completed: March 14, 2003, 20:44:19  
 Job time : 9.33047 secs

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 3.51003 Seconds

(Without alignments)  
1342.037 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49

Sequence: 1 NYKGNVLINIKRCKDDEF.....PDNTYEYKIDNSQVESGSLE 49

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	49	100.0	416 1 S06763	calreticulin precu
2	49	100.0	416 2 JH0819	calreticulin precu
3	49	100.0	417 1 A37047	calreticulin precu
4	49	100.0	418 1 A34154	calreticulin precu
5	30	61.2	400 2 S43376	calreticulin, brai
6	30	61.2	421 2 S36799	calreticulin precu
7	22	44.9	384 2 S29130	calreticulin (clon
8	22	44.9	411 2 S29129	calreticulin precu
9	20	40.8	419 2 S71343	calreticulin precu
10	19	38.8	405 1 JH0795	calreticulin precu
11	13	26.5	406 2 A56637	calreticulin homol
12	9	18.4	336 2 A32507	41K larval antigen
13	9	18.4	395 2 S25851	calreticulin precu
14	8	16.3	393 1 A48573	calreticulin autoa
15	7	14.3	358 2 T12850	hypothetical prote
16	7	14.3	397 2 C75182	DNA-directed RNA p
17	7	14.3	397 2 G71031	probable DNA-direc
18	7	14.3	414 2 T39450	phosphoglycerate k
19	7	14.3	591 2 B54354	calnexin precursor
20	7	14.3	591 2 C54354	calnexin precursor
21	7	14.3	592 2 I53260	calnexin - human
22	7	14.3	592 2 A46673	calnexin precursor
23	7	14.3	593 1 A37273	calnexin precursor
24	7	14.3	1461 2 E84589	probable retroelem
25	6	12.2	19 2 S54848	succinyl-CoA synth
26	6	12.2	81 2 F97347	transition state r
27	6	12.2	97 2 H69440	ribosomal protein
28	6	12.2	103 2 F75010	hypothetical prote
29	6	12.2	109 2 E64473	DNA-directed RNA p

30	6	12.2	144 2 A96580	hypothetical prote
31	6	12.2	146 2 S66060	year protein - Bac
32	6	12.2	152 2 T18975	hypothetical prote
33	6	12.2	160 2 C64279	hypothetical prote
34	6	12.2	173 2 AC3503	nickel-cobalt-cadm
35	6	12.2	187 2 T25461	hypothetical prote
36	6	12.2	196 2 S63429	C151 protein - Yea
37	6	12.2	203 2 H96525	probable terpene c
38	6	12.2	214 2 I49758	hypoxanthine phosph
39	6	12.2	218 1 RTMUG	hypoxanthine phosph
40	6	12.2	218 1 RTMSG	hypoxanthine phosph
41	6	12.2	218 1 RTHYG	hypoxanthine phosph
42	6	12.2	218 1 S43043	hypoxanthine (guan
43	6	12.2	218 2 S21474	hypoxanthine phosph
44	6	12.2	218 2 I51842	hypoxanthine phosph
45	6	12.2	218 2 S18140	hypoxanthine phosph

## ALIGNMENTS

RESULT 1  
S06763  
calreticulin precursor - mouse  
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S06763; JCI1444; PGI233; A57498  
R:Smith, M.J.; Koch, G.L.E.  
EMBO J. 8, 3581-3586, 1989  
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HMCBP), a  
A:Reference number: S06763; MUID:90059955; PMID:2583110  
A:Accession: S06763  
A:Molecule type: DNA  
A:Residues: 1-416 <SMT>  
A:Cross-references: EMBL:X14926; NID:G50567; PIDN:CAA33053.1; PID:G50568  
R:Mazatella, R.A.; Gold, P.; Cunningham, M.; Green, M.  
Gene 120, 217-225, 1992  
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca  
A:Reference number: JCI1444; MUID:93013037; PMID:1398135  
A:Accession: JCI1444  
A:Molecule type: mRNA  
A:Residues: 1-416 <MAZ>  
A:Cross-references: GB:M92988; NID:G193084; PIDN:AAA37569.1; PID:G193085  
A:Accession: PGI233  
A:Molecule type: protein  
A:Residues: 18-41 <MAZ>  
R:White, T.K.; Zhu, O.; Tanzer, M.L.  
J. Biol. Chem. 270, 15926-15929, 1995  
A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mous  
A:Reference number: A57498; MUID:95332280; PMID:7608143  
A:Accession: A57498  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 74-80;142-151;186-193 <WHT>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calregulin #status experimental <MAT>  
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 49; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 6;Se-44;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYKGNVLINIKRCKDDEFTHLYLIVPDPWTYEYKIDNSQVESGSLE 49  
Db 149 NYKGNVLINIKRCKDDEFTHLYLIVPDPWTYEYKIDNSQVESGSLE 197

RESULT 2  
JH0819  
calreticulin precursor - rat



A:Molecule type: protein  
A:Residues: 18-34, 'R' <ROJ>  
R.Krause, K.H.; Slammerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the ER chaperone BiP  
A:Reference number: S11475; MUID:90380058; PMID:2400400  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R.Lamerlin, J.; McCreedy, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.  
submitted to the EMBL Data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region  
A:Reference number: Z22906  
A:Accession: T45075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAM>  
A:Cross-references: EMBL:AD000092; PIDN:AA51176.1  
A:Experimental source: cell line 5H2-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and C:Genetics:  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3  
A:Note: CRIC  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <MT>  
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 49; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 6.3e-44;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 49  
DB 149 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 197

## RESULT 4

A34154  
calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34154; S13047  
R.Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA  
A:Reference number: A34154; MUID:90094320; PMID:2600080  
A:Accession: A34154  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <FLI>  
A:Cross-references: GB:J05138; NID:g164858; PIDN:AA31188.1; PTD:g164859  
R.Tieves, S.; de Mattei, M.; Lanfredit, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A:Reference number: S13045; MUID:91054414; PMID:2241926  
A:Accession: S13047  
A:Molecule type: protein  
A:Residues: 19-32 <TRF>  
C:Superfamily: calreticulin  
C:Keywords: skeletal muscle  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 49; DB 1; Length 418;  
Best Local Similarity 100.0%; Pred. No. 6.3e-44;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 49

DB 149 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 197

## RESULT 5

S43376  
calreticulin, brain isoform 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
C:Accession: S43376; S36801  
R.Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isebe, T.  
Biochem. J. 298, 435-442, 1994  
A:Title: Covalent structure of bovine brain calreticulin.  
A:Reference number: S43376; MUID:94183174; PMID:8135753  
A:Accession: S43376  
A:Molecule type: protein  
A:Residues: 1-400 <MAT>  
A:Experimental source: brain  
R.Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin  
A:Reference number: S36799; MUID:93385184; PMID:8373827  
A:Accession: S36801  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 45-63, 'E', 65-83 <LID>  
A:Experimental source: brain, clone 8.1  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:397-400/Region: endoplasmic reticulum retention signal  
F:120-146/Disulfide bonds: #status experimental  
F:162/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 61.2%; Score 30; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 6.5e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRP 30  
DB 132 NYKGNVLIINKDIRCKDDEFTLTYLIVRP 161

## RESULT 6

S36799  
calreticulin precursor, brain isoform 2 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 13-Aug-1999  
C:Accession: S36799; S36800  
R.Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin  
A:Reference number: S36799; MUID:93385184; PMID:8373827  
A:Accession: S36799  
A:Molecule type: mRNA  
A:Residues: 1-421 <LID>  
A:Cross-references: GB:U13462; NID:g348693; PIDN:AA37307.1; PTD:g348694  
A:Experimental source: brain, clone 9.4  
A:Accession: S36800  
A:Molecule type: protein  
A:Residues: 35-45 <LID>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>  
F:418-421/Region: endoplasmic reticulum retention signal  
F:141-167/Disulfide bonds: #status predicted  
F:183/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 61.2%; Score 30; DB 2; Length 421;  
Best Local Similarity 100.0%; Pred. No. 6.8e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRP 30

DB 153 MKGNVLINKDIRKDEFTHTLIVRP 182  
|||||  
RESULT 7  
S29130  
calreticulin (clone 8) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29130; T01068  
R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997; PMID:1445218  
A:Accession: S29130  
A:Molecule type: mRNA  
A:Residues: 1-384 <TR>  
A:Cross-references: EMBL:X67598  
A:Accession: T01068  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-339, 'XTGR' <TR>  
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611  
A:Experimental source: CNS  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:381-384/Region: endoplasmic reticulum retention signal  
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 44.9%; Score 22; DB 2; Length 384;  
Best Local Similarity 100.0%; Pred. No. 1.7e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 20 FTHLYTLIVRPDNTYEKIDNS 41  
|||||  
DB 140 FTHLYTLIVRPDNTYEKIDNS 161  
RESULT 8  
S29129  
calreticulin precursor (clone 3) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29129  
R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997; PMID:1445218  
A:Accession: S29129  
A:Molecule type: mRNA  
A:Residues: 1-411 <TR>  
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-411/Product: calreticulin #status predicted <MAT>  
F:408-411/Region: endoplasmic reticulum retention signal  
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 44.9%; Score 22; DB 2; Length 411;  
Best Local Similarity 100.0%; Pred. No. 1.8e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 20 FTHLYTLIVRPDNTYEKIDNS 41  
|||||  
DB 163 FTHLYTLIVRPDNTYEKIDNS 184  
RESULT 9  
S71343  
calreticulin precursor - Korean frog  
C:Species: Rana rugosa (Korean frog)  
C:Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Jun-2000

C:Accession: S71343  
R:Yamamoto, S.; Nakamura, M.  
FEBS Lett. 387, 27-32, 1996  
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa  
A:Reference number: S71342; MUID:96234004; PMID:8654561  
A:Accession: S71343  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-419 <YAM>  
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BA11425.1; PID:g1514957  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:19-419/Product: calreticulin #status predicted <MAT>  
F:205-213/Region: nuclear location signal  
F:415-418/Region: endoplasmic reticulum retention signal  
Query Match 40.8%; Score 20; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 2.4e-13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 22 HLYTLIVRPDNTYEKIDNS 41  
|||||  
DB 171 HLYTLIVRPDNTYEKIDNS 190  
RESULT 10  
JH0795  
calreticulin precursor - California sea hare  
N:Alternate names: protein 407  
C:Species: Aplysia californica (California sea hare)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JH0795; B31409; F60977  
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.  
Neuron 9, 1013-1024, 1992  
A:Title: Long-term sensitization training in aplysia leads to an increase in calretic  
A:Reference number: JH0795; MUID:9308937; PMID:1463604  
A:Accession: JH0795  
A:Molecule type: mRNA  
A:Residues: 1-405 <KEN>  
A:Cross-references: GB:S51239; NID:g262053; PIDN:AAB24569.1; PID:g262054  
A:Experimental source: abdominal ganglion and anterial nervous system  
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988  
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion  
tion in Aplysia.  
A:Reference number: A94207; MUID:88320566; PMID:3413132  
A:Accession: B31409  
A:Molecule type: protein  
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>  
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>  
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,  
Electrophoresis 10, 152-157, 1989  
A:Title: Development of a database of amino acid sequences for proteins identified an  
A:Reference number: A60977; MUID:89276264; PMID:2731514  
A:Accession: F60977  
A:Molecule type: protein  
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>  
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-405/Product: calreticulin #status experimental <MAT>  
F:402-405/Region: endoplasmic reticulum retention signal  
Query Match 38.8%; Score 19; DB 1; Length 405;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 22 HLYTLIVRPDNTYEKIDN 40  
|||||  
DB 166 HLYTLIVRPDNTYEKIDN 184  
RESULT 11



A56637  
calreticulin homolog precursor - fruit fly (*Drosophila melanogaster*)  
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog  
C:Species: *Drosophila melanogaster*  
C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
C:Accession: A56637; A37158  
R:Smith, M.J.  
DNA Seq. 3, 247-250, 1992  
A:Title: Nucleotide sequence of a *Drosophila melanogaster* gene encoding a calreticulin  
A:Reference number: A56637; MUID:93208374; PMID:1296819  
A:Accession: A56637  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-406 <SMID>  
A:Cross-references: GB:64461; NID:97685; PIDN:CAA5791.1; PID:97686  
A:Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIPI:128275)  
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Southeimer, R.D.; Capra, J.D.  
J. Clin. Invest. 86, 332-335, 1990  
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom  
A:Reference number: A37158; MUID:90307981; PMID:2365822  
A:Accession: A37158  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: DNA  
A:Residues: 91-105, 'A', 107, 109-124; 182-183, 'L', 185-220 <MCC>  
C:Genetics:  
A:Gene: FlyBase:Crc  
A:Cross-references: FlyBase:FBgn0005585  
A:Introns: 65/1; 222/3  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 26.5%; Score 13; DB 2; Length 406;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YTLIVRPDNTYEV 36  
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Db 172 YTLIVRPDNTYEV 184

RESULT 12  
A32507  
41k larval antigen - nematode (*Onchocerca volvulus*) (fragment)  
C:Species: *Onchocerca volvulus*  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 12-Apr-1995  
C:Accession: A32507; A28813  
R:Umansh, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.  
J. Clin. Invest. 82, 262-269, 1988  
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of  
A:Reference number: A92769; MUID:88273584; PMID:2455736  
A:Accession: A32507  
A:Molecule type: mRNA  
A:Residues: 1-336 <UNN>  
C:Superfamily: calreticulin

Query Match 18.4%; Score 9; DB 2; Length 336;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FTHLYTLIV 28  
|||||  
Db 114 FTHLYTLIV 122

RESULT 13  
S25851  
calreticulin precursor - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S25851; T33996  
R:Smith, M.J.

DNA Seq. 2, 235-240, 1992  
A:Title: A *C. elegans* gene encodes a protein homologous to mammalian calreticulin.  
A:Reference number: S25851; MUID:9329978; PMID:1627827  
A:Accession: S25851  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <SMID>  
A:Cross-references: EMBL:X59589; NID:96693; PIDN:CAA42159.1; PID:96694  
R:Bauer, C.; Courtney, L.; Lapiant, Y.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of *C. elegans* cosmid Y38A10A.  
A:Reference number: 221453  
A:Accession: T33996  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-395 <BAU>  
A:Cross-references: EMBL:AF125963; PIDN:AA14746.1; GSPDB:GND0023; CESP:Y38A10A.5  
A:Experimental source: strain Bristol N2; clone Y38A10A  
C:Genetics:  
A:Gene: CESP:Y38A10A.5  
A:Map position: 5  
A:Introns: 107/3; 315/3  
C:Superfamily: calreticulin  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 18.4%; Score 9; DB 2; Length 395;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 DNTYEVKID 39  
|||||  
Db 174 DNTYEVKID 182

RESULT 14  
A48573  
calreticulin autoantigen homolog precursor - fluke (*Schistosoma mansoni*)  
C:Species: *Schistosoma mansoni*  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48573  
R:Khaliq, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.  
Mol. Biochem. Parasitol. 57, 193-202, 1993  
A:Title: Cloning of the gene encoding a *Schistosoma mansoni* antigen homologous to hum  
A:Reference number: A48573; MUID:93165070; PMID:8433712  
A:Accession: A48573  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-393 <KHA>  
A:Cross-references: GB:M93097; NID:9160928  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBIPI:125086)  
C:Superfamily: calreticulin  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 16.3%; Score 8; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 THLYTLIV 28  
|||||  
Db 167 THLYTLIV 174

RESULT 15  
T12850  
hypothetical protein yopp - *Bacillus subtilis* phage SPBC2  
C:Species: *Bacillus subtilis* phage SPBC2  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 15-Oct-1999  
C:Accession: T12850; F6917  
R:Lazarovic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Meuel, C.; Karamata, D.  
submitted to the EMBL Data Library, August 1997

A:Description: The complete nucleotide sequence of the *Bacillus subtilis* spbetac2 prophage  
 A:Reference number: 217583  
 A:Accession: F12850  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-358 <LAZ>  
 A:Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025564; PIDN:AC13059.1  
 R:kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funo, S.; Galizzi, A.; Gall  
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
 koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
 Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: F69917  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-358 <KUN>  
 A:Cross-references: GB:299114; GB:299115; GB:AL009126; NID:g2634478; PIDN:CAB13999.1; PI  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: yopp

Query Match	14.3%	Score 7;	DB 2;	Length 358;
Best Local Similarity	100.0%	Pred. No. 11;		
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY 8 LINKDIR 14				
Db 21 LINKDIR 27				

Search completed: March 14, 2003, 20:49:01  
 Job time : 4.51003 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 1.87202 Seconds

(without alignments)  
1085.643 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49  
Sequence: 1 NYGKKNVLINKDIRCKDEF.....PDNTYEKIDNSQVESGSL 49

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	416	1	CRTC_MOUSE
2	49	100.0	416	1	CRTC_MOUSE
3	49	100.0	417	1	CRTC_HUMAN
4	49	100.0	418	1	CRTC_RABIT
5	40	61.2	400	1	CRT1_BOVIN
6	30	61.2	421	1	CRT2_BOVIN
7	13	26.5	406	1	CRTC_DROME
8	9	18.4	388	1	RAL1_ONCVO
9	9	18.4	395	1	CRTC_CARL
10	8	16.3	393	1	CRTC_SCHMA
11	7	14.3	397	1	RPA2_PYRAB
12	7	14.3	397	1	RPA2_PYRAB
13	7	14.3	397	1	RPA2_PYRAB
14	7	14.3	414	1	PGK_SCHPO
15	7	14.3	591	1	CALX_MOUSE
16	7	14.3	591	1	CALX_MOUSE
17	7	14.3	592	1	CALX_MOUSE
18	7	14.3	593	1	CALX_MOUSE
19	6	12.2	62	1	MPK3_XENLA
20	6	12.2	109	1	RPL1_ARCFU
21	6	12.2	109	1	RPL1_ARCFU
22	6	12.2	146	1	YAAK_BACSU
23	6	12.2	213	1	HPRT_MOUSE
24	6	12.2	217	1	HPRT_MOUSE
25	6	12.2	217	1	HPRT_MOUSE
26	6	12.2	217	1	HPRT_MOUSE
27	6	12.2	217	1	HPRT_MOUSE
28	6	12.2	218	1	HPRT_MOUSE
29	6	12.2	218	1	HPRT_MOUSE
30	6	12.2	222	1	DSBA_KLEPN
31	6	12.2	226	1	VATE_HETSC
32	6	12.2	233	1	RNC_COXBU
33	6	12.2	235	1	X381_MYCPN

34	6	12.2	269	1	EL2_BOVIN	Q29461 bos taurus
35	6	12.2	295	1	PIP_THEVO	Q97476 thermoplas
36	6	12.2	295	1	SUCD_PSEAE	Q51567 pseudomonas
37	6	12.2	312	1	OXB2_HUMAN	Q97501 homo sapien
38	6	12.2	314	1	MPK3_MOUSE	Q09110 mus musculu
39	6	12.2	318	1	MPK3_HUMAN	P46734 homo sapien
40	6	12.2	340	1	Y151_PYRHO	O57890 pyrococcus
41	6	12.2	345	1	HMUS_YERPE	O56990 yersinia pe
42	6	12.2	351	1	CD2_HUMAN	P06729 homo sapien
43	6	12.2	371	1	MACA_ECO57	P58410 escherichia
44	6	12.2	371	1	MACA_ECOLI	P75830 escherichia
45	6	12.2	379	1	VP26_YEAST	P40335 saccharomyc

## ALIGNMENTS

RESULT 1  
CRTC\_MOUSE  
ID CRTC\_MOUSE STANDARD: PRT: 416 AA.  
AC P14211;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Calreticulin precursor (CRP55) (Calregulin) (HRCBP) (ERP60).  
GN CALR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.  
RC STRAIN=BAUB/c; TISSUE=Liver;  
RX MEDLINE=90059955; PubMed=2583110;  
RA Smith M.J., Koch G.L.E.;  
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,  
RT HACBP), a major calcium binding ER/SR protein.";  
RL EMO J. 8:3581-3586(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93013037; PubMed=1398135;  
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;  
RT "Determination of the sequence of an expressible cDNA clone encoding  
RT ERP60/calregulin by the use of a novel nested set method.";  
RL Gene 120:217-225(1992).  
RN [3]  
RP SEQUENCE OF 18-38.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
RT using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
-----  
CC EMBL: X14926; CAA33053.1; -;  
CC EMBL: M92988; AAA37569.1; -;  
CC PIR: S06763; S06763.  
CC PIR: JCI444; JCI444.  
CC SWISS-2DPAGE: P14211; MOUSE.  
CC MGD: MGI:88252; Calr.

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DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER-TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT REPEAT 351 407 ASP/GLU/LYS-RICH.
FT DISLFPD 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MM; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLINIKDKDEFTLTYLIVRPDNTYEYKIDNSOVESGSL 49
DB 149 NYKGNVLINIKDKDEFTLTYLIVRPDNTYEYKIDNSOVESGSL 157

RESULT 2
CRTC_RAT STANDARD: PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60) (CALBP)
DE (Calcium-binding protein 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
RA Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
RT the Onchocerca volvulus antigen Rat-1."
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura S., Moriya M., Baba T., Michikawa Y., Yamanohe T., Arai K.,
RA Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
RT the acrosome of rat sperm."
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fuehlekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
RT calreticulin in the endoplasmic reticulum."
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN-Sprague-Dawley;
RX Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Ianfedi M., Villa A., Green N.M.,
RA Macleanan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain."
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN-Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatozoa of rat
RT testis."
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN=LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
RA Kametaki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
RT autoimmunogenic antigens in LEC strain of rats."
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- CAUTION: WAS ORIGINALLY (REF. 2) THOUGHT TO BE D-BETA-
CC HYDROXYBUTYRATE DEHYDROGENASE.
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CC
CC EMBL: D78308; BAA11345.1; -.
CC EMBL: X53363; CAA37446.1; -.
CC EMBL: X13702; CAA31987.1; ALT-SEQ.
CC EMBL: X79327; CAA55890.1; -.
CC PIR: S04867; S04867.
CC PIR: S11205; S11205.
CC PIR: S13045; S13045.
CC PIR: A49176; A49176.
CC PIR: S45036; S45036.
CC PIR: JH0819; JH0819.
CC InterPro: IPR001580; Calreticulin.
CC InterPro: IPR000886; ER-target.
CC Pfam: PF00262; calreticulin; 1.
CC PRINTS: PR00626; CALRETICULIN.
CC PRODOM: PD001866; Calreticulin; 1.
CC PROSITE: PS00014; ER-TARGET; 1.
CC PROSITE: PS00803; CALRETICULIN_1; 1.
CC PROSITE: PS00804; CALRETICULIN_2; 1.
CC PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17

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FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 255 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 297 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFD 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MM; 286713CED31A2970 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLINKDIRCKDEFTHLTYLVRDNTVEYKIDNSQVSGSLE 49
DB 149 NYKGNVLINKDIRCKDEFTHLTYLVRDNTVEYKIDNSQVSGSLE 197

RESULT 3
CRTC_HUMAN STANDARD; PRT; 417 AA.
ID P27797;
AC P27797;
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
OS CAIR OR CRTC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92013129; PubMed-1919005;
RA Rokeach L.A., Haselby J.A., Mellor J.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.;
RT "Characterization of the autoantigen calreticulin.";
RL J. Immunol. 147:3031-3039(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-90237213; PubMed-2332496;
RA McCulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski J.L., Itoh Y., Siciliano M.J., Reichlin M., Sonthelmer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-92129342; PubMed-1733953;
RA McCulliffe D.P., Yang Y.S., Wilson J., Sonthelmer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCreedy P., Stiliwagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

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RP SEQUENCE FROM N.A.
RC TISSUE-Eye, Pancreas, and Skin;
RA Strusberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RX SEQUENCE OF 18-36.
RX MEDLINE-92002034; PubMed-1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dechar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866(1991).
RN [8]
RP SEQUENCE OF 18-32.
RX MEDLINE-90380058; PubMed-2400400;
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RL Biochem. J. 270:545-548(1990).
RN [9]
RP SEQUENCE OF 18-28.
RC TISSUE-Liver;
RX MEDLINE-93162045; PubMed-1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [10]
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RC TISSUE-keratinocytes;
RX MEDLINE-93162043; PubMed-1286667;
RA Rasmussen H.H., Van Damme J., Puype M., Gesser B., Cells J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [11]
RP SEQUENCE OF 18-26.
RC TISSUE-Colon carcinoma;
RX MEDLINE-97295306; PubMed-9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: Was originally (Ref. 2) thought to be the 52 kDa Ro
CC autoantigen.
CC -----
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CC -----
DR EMBL: M84739; AAA51916.1; -
DR EMBL: M32294; AAA56582.1; -
DR EMBL: AY047586; AAL1126.1; -
DR EMBL: AD000092; AAB51176.1; -
DR EMBL: BC002500; AAH02500.1; -
DR EMBL: BC007911; AAH07911.1; -
DR EMBL: BC020493; AAH20493.1; -
DR PIR: A37047; A37047.
DR PIR: S11475; S11475.
DR PIR: A42330; A42330.
DR PIR: A46452; A46452.

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DR SWISS-2DPAGE; P27797; HUMAN.  
 DR Aairus/Ghent-2DPAGE; 9401; IEF.  
 DR PMMA-2DPAGE; P27797; -.  
 DR PHCI-2DPAGE; P27797; -.  
 DR HSC-2DPAGE; P27797; HUMAN.  
 DR Slena-2DPAGE; P27797; -.  
 DR Genew; HGNC:1455; CALR.  
 DR MIM; 109091; -.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR Prodom; PD00186; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 417 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT REPEAT 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 273 283 2-1.  
 FT REPEAT 287 297 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 FT SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;  
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Query Match 100.0%; Score 49; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-44;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLINKDIRCKDDEFTLHYTLVPRDNYEYKINSQVSGSLE 49  
 Db 149 NYKGNVLINKDIRCKDDEFTLHYTLVPRDNYEYKINSQVSGSLE 197

RESULT 4  
 CRTC\_RABIT ID STANDARD: PRT: 418 AA.  
 AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin precursor (CRP5) (Calregulin) (HACBP) (ERP60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Slow-twitch skeletal muscle;  
 RX MEDLINE=90094320; PubMed=2600080;  
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;  
 RT "Molecular cloning of the high affinity calcium-binding protein  
 (calreticulin) of skeletal muscle sarcoplasmic reticulum.";  
 RL J. Biol. Chem. 264:21522-21528(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fast-twitch skeletal muscle;  
 RX MEDLINE=91282795; PubMed=2059224;  
 RA Fliegel L., Michalak M.;

RT "Fast-twitch and slow-twitch skeletal muscles express the same  
 RT isoform of calreticulin.";  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 RN [3]  
 RP SEQUENCE OF 18-36.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [4]  
 RP SEQUENCE OF 18-46.  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Ops M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum.";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=92002038; PubMed=1911780;  
 RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 RT monooxygenase and calreticulin.";  
 RL Biochemistry 30:9892-9900(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; J05138; AAA31188.1; -  
 DR PIR; A34154; A34154.  
 DR PIR; C33208; C33208.  
 DR PIR; D33208; D33208.  
 DR PIR; E33208; E33208.  
 DR PIR; E33208; E33208.  
 DR PIR; S13046; S13046.  
 DR PIR; S13047; S13047.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR Prodom; PD00186; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 418 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 418 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT REPEAT 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 273 283 2-1.  
 FT REPEAT 287 297 2-2.

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FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLIINDIRCKDDEFTLTYLVRPNTYEKIDNSQVSGSLE 49
Db 149 NYKGNVLIINDIRCKDDEFTLTYLVRPNTYEKIDNSQVSGSLE 197

RESULT 5
CRTL_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DF 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94183174; PubMed=8135753;
RA Matsuka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isebe T.;
RT "Covalent structure of bovine brain calreticulin."
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin, 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin, 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.
FT CHAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146
FT CARBOHYD 162 162
FT SITE 397 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEB1 CRC64;

Query Match 61.2%; Score 30; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 NYKGNVLIINDIRCKDDEFTLTYLVRP 30
Db 132 NYKGNVLIINDIRCKDDEFTLTYLVRP 161

RESULT 6
CRTL_BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1998 (Rel. 36, last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin."
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL: L13462; AAC37307.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin, 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin, 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT DOMAIN 35 201 N-DOMAIN.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.
FT REPEAT 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 195 206 1-1.
FT REPEAT 214 225 1-2.
FT REPEAT 231 242 1-3.
FT REPEAT 248 259 1-4.
FT REPEAT 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 61.2%; Score 30; DB 1; Length 421;
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Best Local Similarity 100.0%; Pred. No. 3,1e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINRDIRCKDEFTHTLYLTVRP 30  
Db 153 NYKGNVLINRDIRCKDEFTHTLYLTVRP 182

RESULT 7  
CRTC\_DROME STANDARD: PRT: 406 AA.

AC P28413: 09VHA3;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calreticulin precursor (CRP55) (Calregulin) (HMCBP).  
GN CRC OR CG9429.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93208374; PubMed=1296619;  
RA Smith M.J.;  
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a  
RL DNA Seq. 3:247-250(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cavley S., Dahlke C., Davenport I.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zhong X.H., Zhong F.-N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
RN [3]  
RP SEQUENCE OF 91-124 AND 182-220.

RX MEDLINE=90307981; PubMed=2365822;  
RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,  
RA Capra J.D.;  
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
RT highly homologous with oncoferritin RAL-1 antigen and an alypsia  
RT 'memory molecule'";  
RL J. Clin. Invest. 86:332-335(1990).  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
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CC -----  
CC EMBL: X64461; CAA45791.1; -;  
CC EMBL: AE003683; AAF54416.1; -;  
CC PIR: A37158; A37158.  
CC FLYBASE: FBgn0005585; Crc.  
CC InterPro: IPR001580; Calreticulin.  
CC InterPro: IPR000886; ER\_target.  
CC Pfam: PF00262; Calreticulin; 1.  
CC PRINTS: PR00626; Calreticulin.  
CC ProDom: PD001866; Calreticulin; 1.  
CC PROSITE: PS00014; ER\_TARGET; 1.  
CC PROSITE: PS00803; CALRETICULIN\_1; 1.  
CC PROSITE: PS00804; CALRETICULIN\_2; 1.  
CC PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
CC Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
FT SIGNAL 1 17  
FT CHAIN 18 406  
FT CONFLICT 107 107 G->A (IN REF. 3).  
FT CONFLICT 184 184 V->L (IN REF. 3).  
SO SEQUENCE 406 AA; 46808 MW; 65D72C69D0BC427 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 406;  
Best Local Similarity 100.0%; Pred. No. 2,2e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 YTLVIRPNTYEV 36  
Db 172 YTLVIRPNTYEV 184

RESULT 8  
RAL1\_ONCVO STANDARD: PRT: 388 AA.

ID RAL1\_ONCVO  
AC P11012;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE RAL-1 protein precursor (41 Kda larval antigen).  
GN RAL1.  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94341871; PubMed=7520419;  
RA Rokeach I.A., Zimmerman P.A., Unnasch T.R.;  
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the  
RT calreticulin family of proteins, recognized by sera from patients  
RT with onchocerciasis";  
RL Infect. Immun. 62:3696-3704(1994).  
RN [2]  
RP SEQUENCE OF 53-388 FROM N.A.  
RX MEDLINE=88273584; PubMed=2455736;



RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;  
 RT "Isolation and characterization of expression cDNA clones encoding  
 RT antigens of *Onchocerca volvulus* infective larvae.";  
 RL J. Clin. Invest. 82:262-269(1988).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M20565; AAA59056.1; -  
 DR PIR: A32507; A32507.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR KAM: K00805; CALRETICULIN\_REPEAT; 3.  
 KW Calcium-binding; Repeat; Antigen; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 388 RAL-1 PROTEIN.  
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
 FT REPEAT 189 200 1-1.  
 FT REPEAT 208 219 1-2.  
 FT REPEAT 225 236 1-3.  
 FT REPEAT 242 253 1-4.  
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
 FT REPEAT 257 267 2-1.  
 FT REPEAT 271 281 2-2.  
 FT REPEAT 285 295 2-3.  
 FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
 FT DISULFID 135 161 BY SIMILARITY.  
 SQ SEQUENCE 388 AA; 45298 MW; 9537E298A2D31CD6 CRC64;

Query Match 18.4%; Score 9; DB 1; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FTHLYTLIV 28  
 DB 166 FTHLYTLIV 174

RESULT 9  
 CRTC\_CAEEL STANDARD: PRT: 395 AA.  
 AC P27798;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Calreticulin precursor.  
 GN CRT-1 OR Y38A10A.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabditiida; Rhabditoidea;  
 OC Rhabditiidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RX MEDLINE=92329978; PubMed=1627827;  
 RA Smith M.J.;  
 RT "A. C. elegans gene encodes a protein homologous to mammalian  
 RT calreticulin.";  
 RL DNA Seq. 2:235-240(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RX Bauer C., Courtney L., Lapiant Y.;

RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP REVISIONS.  
 RA Waterston R.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X59589; CAA42159.1; -  
 DR EMBL: AF125963; AAD14746.1; -  
 DR PIR: S25851; S25851.  
 DR WormDep: Y38A10A.5; CE21562.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 15  
 FT CHAIN 16 395  
 FT DOMAIN 16 192 N-DOMAIN.  
 FT DOMAIN 193 301 P-DOMAIN.  
 FT DOMAIN 302 395 C-DOMAIN.  
 FT DOMAIN 186 250 4 X APPROXIMATE REPEATS.  
 FT REPEAT 186 197 1-1.  
 FT REPEAT 205 216 1-2.  
 FT REPEAT 222 233 1-3.  
 FT REPEAT 239 250 1-4.  
 FT DOMAIN 254 292 3 X APPROXIMATE REPEATS.  
 FT REPEAT 254 264 2-1.  
 FT REPEAT 268 278 2-2.  
 FT REPEAT 282 292 2-3.  
 FT DOMAIN 332 390 ASP/GLU/LYS-RICH.  
 FT DISULFID 133 158 BY SIMILARITY.  
 FT SITE 392 395 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;

Query Match 18.4%; Score 9; DB 1; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 0.035;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 DNTYEYKID 39  
 DB 174 DNTYEYKID 182

RESULT 10  
 CRTC\_SCHMA STANDARD: PRT: 393 AA.  
 AC Q06814; Q26562;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Calreticulin precursor (SM4 protein).  
 GN Schistosoma mansoni (Blood fluke).  
 OS Schistosoma mansoni.  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OC NCBI\_TaxID=6183;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-Puerto Rican;  
 RX MEDLINE-93165070; PubMed-8433712;  
 RA Khalife J., Troltein F., Schacht A.-M., Godin C., Pierce R.J.,  
 RA Capron A.;  
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen  
 RT homologous to human Ro/SS-A autoantigen";  
 RL Mol. Biochem. Parasitol. 57:193-202(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Puerto Rican;  
 RX MEDLINE-94187805; PubMed-8139623;  
 RA Khalife J., Pierce R.J., Godin C., Capron A.;  
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni  
 RT calreticulin";  
 RL Mol. Biochem. Parasitol. 62:313-315(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M93097; AAA29854.1; -  
 DR EMBL: L24159; AAA19024.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 KW SIGNAL  
 FT CHAIN 1 16  
 FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.  
 FT REPEAT 189 200 1-1.  
 FT REPEAT 209 220 1-2.  
 FT REPEAT 225 236 1-3.  
 FT REPEAT 243 254 1-4.  
 FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.  
 FT REPEAT 257 267 2-1.  
 FT REPEAT 271 281 2-2.  
 FT REPEAT 285 295 2-3.  
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 135 161 BY SIMILARITY.  
 FT SITE 390 393 PREVENT SECRETION FROM ER.  
 FT CONFLICT 89 90 MY -> IL (IN REF. 2).  
 FT CONFLICT 188 207 MISSING (IN REF. 2).  
 FT CONFLICT 378 378 Y -> D (IN REF. 2).  
 SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 16.3%; Score 8; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 YLTYLTV 28  
 |||||||  
 DB 167 YLTYLTV 174

RESULT 11  
 ID RPA2-PYRAB STANDARD; PRT: 397 AA.  
 AC Q9V113;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).  
 GN RPOA2 OR PAB0425  
 OS Pyrococcus abyssi  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID-29292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CE5 / Orsay;  
 RA Helling R.;  
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
 RT structure and evolution";  
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
 CC SUBSTRATES.  
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC (RNA)(N).  
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AJ248284; CAB49538.1; -  
 DR InterPro: IPR002879; RNA\_pol\_A2.  
 DR Pfam: PF01854; RNA\_pol\_A2; 1.  
 DR Transference; Transcription; DNA-directed RNA polymerase;  
 KW Complete proteome.  
 SQ SEQUENCE 397 AA; 44594 MW; E459658EA9C15CB CRC64;

Query Match 14.3%; Score 7; DB 1; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YLTYVRP 30  
 |||||||  
 DB 198 YLTYVRP 204

RESULT 12  
 ID RPA2-PYRAB STANDARD; PRT: 397 AA.  
 AC Q800M5;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).  
 GN RPOA2 OR PFI562.  
 OS Pyrococcus furiosus.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID-2261;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;  
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;  
 RT "The complete sequence of the Pyrococcus furiosus genome";  
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription  
 CC of DNA into RNA using the four ribonucleoside triphosphates as  
 CC substrates.  
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC (RNA)(N).  
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
 CC -----

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CC -----  
DR EMBL: AE010257; AAL81686.1; -  
KW Complete proteome.  
SQ SEQUENCE 397 AA; 44404 MW; 19D46E356CA0E49F CRC64;  
  
Query Match 14.3%; Score 7; DB 1; Length 397;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 24 YTLIVRP 30  
Db 198 YTLIVRP 204  
|||||  
Db 198 YTLIVRP 204  
  
RESULT 13  
RPA2\_PYRHO STANDARD; PRT; 397 AA.  
ID RPA2\_PYRHO  
AC 093777;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE DNA-directed RNA polymerase subunit A\* (EC 2.7.7.6).  
GN RPOA2 OR PH1544.  
OS Pyrococcus horikoshii.  
OC Archaea: Euryarchaeota: Thermococci: Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OT3;  
RX MEDLINE=98344137; PubMed=9679194;  
RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kusuda N., Oguchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuho Y., Shizuya H., Kikuchi H.;  
RT Complete sequence and gene organization of the genome of a hyper-  
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
RL DNA Res. 5:55-76(1998).  
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
CC SUBSTRATES.  
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate + N diphosphate +  
CC (RNA)(N).  
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
CC -----  
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CC -----  
DR EMBL: AP000066; BAA30655.1; -  
DR InterPro: IPR002879; RNA\_pol\_A2.  
DR Pfam: PF01854; RNA\_pol\_A2; 1.  
KW Transferase: Transcription; DNA-directed RNA polymerase;  
KW Complete proteome.  
SQ SEQUENCE 397 AA; 44507 MW; 7846655AB5D4730D CRC64;  
  
Query Match 14.3%; Score 7; DB 1; Length 397;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 YTLIVRP 30  
Db 198 YTLIVRP 204  
|||||  
Db 198 YTLIVRP 204  
  
RESULT 14  
PGK\_SCHPO STANDARD; PRT; 414 AA.  
ID PGK\_SCHPO  
AC 060101;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Phosphoglycerate kinase (EC 2.7.2.3).  
GN PGK1 OR SPBCL4F5.04C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,  
RA Gattles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Travey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Voickert G., Aert R., Robben J., Gymnopoulos B.,  
RA Weltjens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Filz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,  
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880(2002).  
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate - ADP + 3-  
CC phospho-D-glyceroyl phosphate.  
CC -1- PATHWAY: Second phase of glycolysis: second step.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.  
CC -----  
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CC -----  
DR EMBL: AL023780; CAA19322.1; -  
DR HSP: P00560; 10PG.  
DR InterPro: IPR001576; PGK.  
DR Pfam: PF00162; PGK; 1.  
DR PRINTS: PR00477; PGK1CKINASE.  
DR PROSITE: PS00111; GLYCERATE\_KINASE; 1.  
KW Transferase: Kinase; GLYCOLYSIS.  
SQ SEQUENCE 414 AA; 43964 MW; F40D706D5487B4E CRC64;

Query Match 14.3%; Score 7; DB 1; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 4.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 3 KGNVLI 9  
 |||||  
 Db 15 KGNVLI 21

## RESULT 15

CALX\_MOUSE STANDARD: PRT: 591 AA.  
 AC P35564; 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calnexin precursor.  
 GN CANX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94183823; PubMed=8136357;  
 RA Tjoelker L.W., Seyfried C.E., Eddy R.L. Jr., Shows T.B. Jr.,  
 RA Calderon J., Schreiber R.B., Gray P.W.;  
 RT "Human, mouse, and rat calnexin cDNA cloning: identification of  
 potential calcium binding motifs and gene localization to human  
 chromosome 5.";  
 RT Biochemistry 33:3229-3236(1994).  
 RL [2]  
 RN SEQUENCE OF 21-591 FROM N.A.  
 RP STRAIN-BALB/C;  
 RX MEDLINE=94198223; PubMed=8148318;  
 RA Schreiber K.L., Bell M.P., Huntoon C.J., Rajagopalan S.,  
 RA Brenner M.B., Mckean D.J.;  
 RT "Class II histocompatibility molecules associate with calnexin during  
 assembly in the endoplasmic reticulum.";  
 RL Int. Immunol. 6:101-111(1994).  
 CC -1- FUNCTION: CALCIUM-BINDING PROTEIN THAT INTERACTS WITH NEWLY  
 SYNTHESIZED GLYCOPROTEINS IN THE ENDOPLASMIC RETICULUM. IT MAY ACT  
 IN ASSISTING PROTEIN ASSEMBLY AND/OR IN THE RETENTION WITHIN THE  
 ER OF UNASSEMBLED PROTEIN SUBUNITS. IT SEEMS TO PLAY A MAJOR ROLE  
 IN THE QUALITY CONTROL APPARATUS OF THE ER BY THE RETENTION OF  
 INCORRECTLY FOLDED PROTEINS.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic  
 reticulum.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L18888; AAA21014.1; -;  
 DR EMBL: L23865; AAA62450.1; -;  
 DR MGD; MGI:88261; Canx.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PRO0626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Calcium-binding; Endoplasmic reticulum; Transmembrane; Signal;  
 KW Repeat; Chaperone.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 591 CALNEXIN.  
 FT DOMAIN 21 463 LUMENAL (POTENTIAL).

FT TRANSMEM 483 503 POTENTIAL.  
 FT DOMAIN 504 591 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 279 346 4 X APPROXIMATE REPEATS.  
 FT REPEAT 279 291 1-1.  
 FT REPEAT 296 308 1-2.  
 FT REPEAT 315 327 1-3.  
 FT REPEAT 334 346 1-4.  
 FT DOMAIN 349 406 4 X APPROXIMATE REPEATS.  
 FT REPEAT 349 359 2-1.  
 FT REPEAT 368 378 2-2.  
 FT REPEAT 382 392 2-3.  
 FT REPEAT 396 406 2-4.  
 FT CONFLICT 416 416 K -> R (IN REF. 2).  
 FT CONFLICT 468 468 P -> L (IN REF. 2).  
 FT CONFLICT 472 472 L -> G (IN REF. 2).  
 FT CONFLICT 538 538 R -> G (IN REF. 2).  
 FT CONFLICT 560 560 V -> G (IN REF. 2).  
 SQ SEQUENCE 591 AA: 67277 MW; 0D9F8FE03434BADC CAC64;

Query Match 14.3%; Score 7; DB 1; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 6.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 21 THLYTLI 27  
 |||||  
 Db 236 THLYTLI 242

Search completed: March 14, 2003, 20:45:08  
 Job time : 2.87202 secs

GenCore version 5.1.4.P5\_4578  
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# OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 6.55205 Seconds  
(without alignments)  
1540.938 Million cell updates/sec

Title: US-09-807-148-6  
Perfect score: 49  
Sequence: 1 NYKGNVINKDIRCKDDEF.....PDNTYEKIDNSQVSSGLE 49

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	61.2	417	6	08SQ53 bos taurus
2	22	44.9	343	13	091711 xenopus lae
3	22	44.9	411	13	091710 xenopus lae
4	20	40.8	419	13	098984 rana rugosa
5	19	38.8	405	5	026268 aplysia cal.
6	18	36.7	421	5	090650 strongyloce
7	14	28.6	214	4	09UDG2 homo sapien
8	13	26.5	395	5	096722 taenia soli
9	13	26.5	406	5	09U916 drosophila
10	12	24.5	318	13	09PTX7 leishenteron
11	12	24.5	350	5	026514 schistosoma
12	12	24.5	396	5	045034 schistosoma
13	12	24.5	559	5	09NG26 tritrichomo
14	11	22.4	406	5	08MR36 anopheles g
15	11	22.4	407	5	08T9U3 aedes aegypt
16	9	18.4	375	5	018478 litomosoides

17	9	18.4	387	5	097372 dirofilaria
18	9	18.4	403	5	076961 necator ame
19	9	18.4	410	5	016893 amblyomma a
20	8	16.3	137	11	09D373 mus musculu
21	8	16.3	380	11	09D9Q6 mus musculu
22	8	16.3	384	4	096LNS homo sapien
23	8	16.3	384	4	096L12 homo sapien
24	8	16.3	397	5	08WPG8 galliera me
25	8	16.3	415	5	08WRU9 meloidogyne
26	8	16.3	417	13	09PUC1 puuci brachydanio
27	7	14.3	215	6	09TSB7 dictyostell
28	7	14.3	231	5	096085 canis sp. b
29	7	14.3	229	17	08U458 plasmodium
30	7	14.3	279	17	08U458 plasmodium
31	7	14.3	280	1	052958 pyrococcus
32	7	14.3	358	9	064099 bacterioph
33	7	14.3	358	16	034336 bacillus su
34	7	14.3	397	17	08U0M5 pyrococcus
35	7	14.3	511	16	08XXY7 raietonia s
36	7	14.3	519	5	08SR76 encaphalito
37	7	14.3	801	10	0942X7 oryza sativ
38	7	14.3	910	10	08VWV9 pinus pinas
39	7	14.3	1373	4	09Y2F5 homo sapien
40	7	14.3	1461	10	09SIM3 arabidopsis
41	6	12.2	76	6	097871 isodon mac
42	6	12.2	76	6	097872 isodon mac
43	6	12.2	76	6	097873 macropus eu
44	6	12.2	76	6	097874 macropus eu
45	6	12.2	76	6	097875 monodelphis

## ALIGNMENTS

RESULT 1	08SQ53	PRELIMINARY:	PRT:	417 AA.
ID	08SQ53			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DR	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DN	Calreticulin.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OX	Bovidae; Bovinae; Bos.			
RY	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hossain M.A., Takawa K., Nakajima H., Nakajima T.;			
RT	"Bovine brain calreticulin."			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AB067687; BAB6913.1; - 7BF812C7B5417BE9 CRC64;			
SQ	SEQUENCE 417 AA, 48038 MW; 7BF812C7B5417BE9 CRC64;			
Query Match	61.2%; Score 30; DB 6; Length 417;			
Best Local Similarity	100.0%; Pred. No. 2e-24;			
Matches	30; Conservative	0; Mismatches	0; Indels	0; Gaps
OY	1 NYKGNVINKDIRCKDDEFTHLYTVLP 30			
DB	149 NYKGNVINKDIRCKDDEFTHLYTVLP 178			
RESULT 2	091711	PRELIMINARY:	PRT:	343 AA.
ID	091711			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DR	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DN	Calreticulin (Fragment).			

OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxId=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=CNS;  
 RA Treves S., Zorzato F., Pozzan T.;  
 RT Identification of calreticulin isoform in the CNS.;  
 RL Biochem. J. 0:0-0(0).  
 DR EMBL: X67598; CAA47867.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER  
 SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 44.9%; Score 22; DB 13; Length 343;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FTHLYTLIVRPDNTYEKIDNS 41  
 DB 140 FTHLYTLIVRPDNTYEKIDNS 161  
 |||||||||||||||||||

RESULT 3  
 ID 091710 PRELIMINARY; PRT; 411 AA.  
 AC 091710;  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-JAN-1998 (TREMBLrel. 19, last annotation update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Calreticulin precursor (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxId=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=CNS;  
 RA Treves S., Zorzato F., Pozzan T.;  
 RT Identification of calreticulin isoform in the CNS.;  
 RL Biochem. J. 0:0-0(0).  
 DR EMBL: X67597; CAA47866.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW Signal.  
 FT NON\_TER  
 FT SIGNAL  
 FT CHAIN  
 SQ SEQUENCE 411 AA; 48344 MW; 891DA66E00EBEFA CRC64;

Query Match 44.9%; Score 22; DB 13; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 1e-15;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FTHLYTLIVRPDNTYEKIDNS 41  
 DB 163 FTHLYTLIVRPDNTYEKIDNS 164  
 |||||||||||||||||||

RESULT 4  
 ID 098984 PRELIMINARY; PRT; 419 AA.  
 AC 098984;  
 DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)  
 DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Calreticulin.  
 OS Rana rugosa (Wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
 OX NCBI\_TaxId=8410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96234004; PubMed=8654561;  
 RA Yamamoto S., Nakamura M.;  
 RT "Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa";  
 RL FEBS Lett. 387:27-32(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96387817; PubMed=8795287;  
 RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;  
 RT "Strong expression of the calreticulin gene in the liver of Rana rugosa tadpoles, but not adult frogs";  
 RL J. Exp. Zool. 275:431-443(1996).  
 DR EMBL: D78589; BAA11425.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 40.8%; Score 20; DB 13; Length 419;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 HLYTLIVRPDNTYEKIDNS 41  
 DB 171 HLYTLIVRPDNTYEKIDNS 190  
 |||||||||||||||||||

RESULT 5  
 ID 026268 PRELIMINARY; PRT; 405 AA.  
 AC 026268;  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Calreticulin.  
 GN CALRETICULIN.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxId=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93098937; PubMed=1463604;  
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein";  
 RL Neuron 9:1013-1024(1992).  
 DR EMBL: S51239; AAB24569.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin.1.

DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; CALRETICULIN.1.  
 DR PROSITE: PS00803; CALRETICULIN.1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN.REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
 SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DID69 CRC64;

Query Match 38.8%; Score 19; DB 5; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-12;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 HLYTLIVRPDNTFEVKIDN 40  
 ||||||||||||||||  
 DB 166 HLYTLIVRPDNTFEVKIDN 184

RESULT 6  
 Q9U6S0 PRELIMINARY; PRT; 421 AA.

AC Q9U6S0:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Calreticulin precursor.  
 GN CALRET.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 CC Echinoidae; Euechinoidae; Echinacea; Echinoida; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Susan J.M., Just W.L., Lemnarz W.J.;  
 RT "Cloning and Characterization of Alpha Integrin and Calreticulin in  
 RT Embryos of the Sea Urchin."  
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF177915; AAD55725.1; -.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; CALRETICULIN.1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN.REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
 KW Signal.  
 FT SIGNAL.  
 FT CHAIN 1 19 POTENTIAL.  
 FT CHAIN 20 421 CALRETICULIN.  
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 36.7%; Score 18; DB 5; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-11;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KDICKNDDEFHLYTLIV 28  
 ||||||||||||||||  
 DB 158 KDICKNDDEFHLYTLIV 175

RESULT 7  
 Q9UDG2 PRELIMINARY; PRT; 214 AA.

AC Q9UDG2:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE CALRETICULIN-CALCIUM binding protein (Fragments).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=95143082; PubMed=7841019;  
 RA Hosen G., Koch C.;  
 RT "Human placental calreticulin: purification, characterization and  
 RT association with other proteins."  
 RL Acta Chem. scand. 48:905-911(1994).  
 DR InterPro: IPR001580; Calreticulin.  
 DR PRODOM: PD001866; Calreticulin.1.  
 FT NON\_TER 1 1  
 FT NON\_CONS 31 32  
 FT NON\_CONS 59 60  
 FT NON\_CONS 78 79  
 FT NON\_CONS 116 117  
 FT NON\_TER 214 214  
 SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 28.6%; Score 14; DB 4; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 VKIDNSQVESGSLF 49  
 ||||||||||||||||  
 DB 95 VKIDNSQVESGSLF 108

RESULT 8  
 ID Q967Z2 PRELIMINARY; PRT; 395 AA.

AC Q967Z2:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Calcium binding protein calreticulin precursor.  
 OS Taenia solium.  
 CC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
 CC Cyclophyllidae; Taeniidae; Taenia.  
 OX NCBI\_TaxID=6204;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mendlovic F., Ostoa-Saloma P., Flisser A., Lacleite J.P.;  
 RT "Molecular characterization of Taenia solium calreticulin."  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF340232; AAK52725.1; -.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRODOM: PD001866; CALRETICULIN.1.  
 DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN.1.  
 DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN.1.  
 DR PROSITE: PS00805; CALRETICULIN.REPEAT; UNKNOWN.1.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
 KW Signal.  
 FT SIGNAL.  
 FT SIGNAL 1 18 POTENTIAL.  
 SQ SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;

Query Match 26.5%; Score 13; DB 5; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 6e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 THLYTLIVRPDNT 33  
 ||||||||||||||||  
 DB 168 THLYTLIVRPDNT 180

RESULT 9  
 Q9U916 PRELIMINARY; PRT; 406 AA.

AC Q9U916:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 GN CRC OR CG9429.

OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OREGON-R;  
 RA Dodo K., Sakoyama Y., Gamo S.;  
 RT "Drosophila melanogaster calreticulin for mRNA."  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB000718; BAA85379.1; -  
 DR Flybase: FBgn005585; Crc.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; Calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 26.5%; Score 13; DB 5; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YTLIVRPDMTYEV 36  
 |||||  
 DB 172 YTLIVRPDMTYEV 184

RESULT 10  
 O9PTX7 PRELIMINARY; PRT; 318 AA.  
 AC O9PTX7;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin (Fragment).  
 OS Leishneron reissneri.  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperartia;  
 OC Petromyzontiformes; Petromyzontidae; Lethenteron.  
 OX NCBI\_TaxID=7753;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:20063780; PubMed-10594174;  
 RA Kuraku S., Hoshiyama D., Kato K., Suga H., Miyata T.;  
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes."  
 RT J. Mol. Evol. 49:729-735(1999).  
 RL EMBL: AB025328; BAA8481.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 318 AA; 36997 MW; C88102EAC1506 CRC64;

Query Match 24.5%; Score 12; DB 13; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LINKDIRCKDE 19  
 |||||  
 DB 55 LINKDIRCKDE 66

RESULT 11  
 ID Q26514 PRELIMINARY; PRT; 350 AA.  
 AC Q26514;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin (Fragment).  
 GN RAL-1.  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CHINESE;  
 RA Huggins M.C., Moloney N.A.;  
 RT "Cloning of a gene encoding a Schistosoma japonicum vaccine candidate with homology to a human Ro/SS-A autoantigen."  
 RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: M80524; AAA29917.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 350 AA; 40385 MW; 30FBA4E8B685D1C CRC64;

Query Match 24.5%; Score 12; DB 5; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 THLYTLIVRPDN 32  
 |||||  
 DB 122 THLYTLIVRPDN 133

RESULT 12  
 ID Q45034 PRELIMINARY; PRT; 396 AA.  
 AC Q45034;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin.  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PHILIPPINE;  
 RX MEDLINE:21165812; PubMed-11269324;  
 RA Scott J.C., McManus D.P.;  
 RT "Molecular cloning and functional expression of a cDNA encoding the major endoplasmic reticulum-associated calcium-binding protein, calreticulin, from Philippine strain Schistosoma japonicum."  
 RT Parasitol. Int. 48:35-46(1999).  
 RL EMBL: AF044408; AAC00515.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.



SQ SEQUENCE 396 AA; 45814 MW; C57394CGFB4CD77B CRC64;  
Query Match 24.5%; Score 12; DB 5; Length 396;  
Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 THLYTLIVRPD 32  
|||||  
DB 168 THLYTLIVRPD 179

RESULT 13  
Q9NG26 PRELIMINARY; PRT; 559 AA.  
AC Q9NG26:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE Calreticulin-like protein precursor.  
OS Trichomonas suis.  
OC Eukaryota; Parabasalidea; Trichomonadida; Trichomonadidae;  
OC Trichomonas.  
OX NCBI\_TaxID=56690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1/N;  
RX MEDLINE=20264030; PubMed-10802323;  
RA Felleisen R.S.J., Hemphill A., Ingold K., Gottstein B.;  
RT "Conservation of calnexin in the early branching protozoan  
Trichomonas suis.";  
RL MOL. Biochem. Parasitol. 108:109-117(2000).  
DR EMBL: A011990; CAB92410.1; -;  
DR Interpro:IPR001580; Calreticulin.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
KW Signal.  
FT SIGNAL 1 13 POTENTIAL.  
SQ SEQUENCE 559 AA; 63303 MW; 863407D8963EE42D CRC64;

Query Match 24.5%; Score 12; DB 5; Length 559;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 THLYTLIVRPD 32  
|||||  
DB 186 THLYTLIVRPD 197

RESULT 14  
Q8MR36 PRELIMINARY; PRT; 406 AA.  
AC Q8MR36:  
DT 01-MAR-2002 (TREMblrel. 20, Created)  
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE Calreticulin.  
OS Anopheles gambiae (African malaria mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
OC Anopheles.  
OX NCBI\_TaxID=7165;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;  
RT "Towards a catalog for genes and proteins from the salivary gland of  
the malaria vector, Anopheles gambiae.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF457551; AAL68781.1; -;  
DR Interpro: IPR001580; Calreticulin.

DR Interpro: IPR000886; ER-target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; UNKNOWN\_1.  
DR PROSITE: PS00804; CALRETICULIN\_2; UNKNOWN\_1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; UNKNOWN\_3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9331F1 CRC64;

Query Match 22.4%; Score 11; DB 5; Length 406;  
Best Local Similarity 100.0%; Pred. No. 0.00092;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LINKDIRCKD 18  
|||||  
DB 153 LINKDIRCKD 163

RESULT 15  
Q8T903 PRELIMINARY; PRT; 407 AA.  
AC Q8T903:  
DT 01-JUN-2002 (TREMblrel. 21, Created)  
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE Putative calreticulin.  
OS Aedes aegypti (Yellowfever mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
OC Aedes.  
OX NCBI\_TaxID=7159;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BLACK EYE; TISSUE=Salivary Gland;  
RA Valenzuela J.G., Pham V.M., Garfield M.K., Francischetti I.M.,  
RA Ribeiro J.M.C.;  
RT "Toward the sialome of the adult female mosquito Aedes aegypti.";  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF466603; AAL76026.1; -;  
SQ SEQUENCE 407 AA; 46773 MW; 25E28C7715DE4338 CRC64;

Query Match 22.4%; Score 11; DB 5; Length 407;  
Best Local Similarity 100.0%; Pred. No. 0.00092;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LINKDIRCKD 18  
|||||  
DB 156 LINKDIRCKD 166

Search completed: March 14, 2003, 20:47:38  
Job time : 6.55205 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 15.7784 Seconds  
(without alignments)  
522.132 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 280

Sequence: 1 GPGRKRVHVFYFNKGNVLI.....EEDKEDEEEDVPGQANDEL 280

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: Issued.Patents-AA:\*  
2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	6.8	19	1	US-08-335-198-10
2	17	6.1	17	1	US-08-045-261-9
3	13	4.6	415	4	US-08-675-816-2
4	11	3.9	542	4	US-08-675-816-6
5	10	3.6	17	1	US-08-335-198-9
6	9	3.2	412	2	US-08-741-134-2
7	8	2.9	369	2	US-08-723-415B-4
8	8	2.9	369	2	US-08-189-627A-4
9	8	2.9	369	4	US-09-710-861-4
10	8	2.9	370	2	US-08-723-415B-6
11	8	2.9	370	4	US-09-188-627A-6
12	8	2.9	370	4	US-09-710-861-6
13	8	2.9	385	2	US-08-723-415B-8
14	8	2.9	385	4	US-09-189-627A-8
15	8	2.9	385	4	US-09-710-861-8
16	8	2.9	444	3	US-09-221-235-14
17	8	2.9	444	3	US-09-221-928-14
18	8	2.9	444	4	US-09-221-527-14
19	8	2.9	444	4	US-09-221-236-14
20	8	2.9	444	4	US-09-221-416-14
21	8	2.9	444	4	US-09-221-245-14
22	8	2.9	444	4	US-09-163-115-14
23	8	2.9	444	4	US-09-221-528-14
24	8	2.9	444	4	US-09-593-553-14
25	8	2.9	444	4	US-09-221-237-14
26	8	2.9	446	2	US-08-723-415B-2
27	8	2.9	446	4	US-09-189-627A-2

28	8	2.9	446	4	US-09-710-861-2	Sequence 2, Appl
29	8	2.9	460	1	US-08-630-592-7	Sequence 7, Appl
30	8	2.9	460	1	US-08-714-991-7	Sequence 7, Appl
31	8	2.9	460	3	US-09-032-365A-8	Sequence 8, Appl
32	8	2.9	506	2	US-08-631-200-8	Sequence 8, Appl
33	8	2.9	506	2	US-08-829-553-8	Sequence 8, Appl
34	8	2.9	506	2	US-08-922-267A-8	Sequence 8, Appl
35	8	2.9	506	2	US-08-936-707A-8	Sequence 8, Appl
36	8	2.9	506	2	US-08-936-706A-8	Sequence 8, Appl
37	8	2.9	506	3	US-09-248-203-8	Sequence 8, Appl
38	8	2.9	506	3	US-09-032-365A-62	Sequence 62, Appl
39	8	2.9	506	4	US-08-812-824-4	Sequence 4, Appl
40	8	2.9	506	4	US-09-406-071-8	Sequence 8, Appl
41	8	2.9	506	4	US-08-955-918C-10	Sequence 10, Appl
42	8	2.9	506	4	US-08-697-766A-10	Sequence 10, Appl
43	8	2.9	512	3	US-09-032-365A-60	Sequence 60, Appl
44	8	2.9	518	3	US-09-032-365A-58	Sequence 58, Appl
45	8	2.9	561	1	US-08-714-991-27	Sequence 27, Appl

#### ALIGNMENTS

RESULT 1  
US-08-335-198-10  
Sequence 10, Application US/08335198  
Patent No. 5637454  
GENERAL INFORMATION:  
APPLICANT: Harley, John B.  
TITLE OF INVENTION: Assays and Treatments for Autoimmune  
TITLE OF INVENTION: Diseases  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Ste. 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309-4539  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,198  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/648205  
FILING DATE: 01-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF 114CIP  
TELEPHONE: (404)815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-335-198-10  
Query Match 6.8%; Score 19; DB 1; length 19;

Best Local Similarity 100.0%; Pred. No. 7.9e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 262 EDKEDEEDVPGQAKDEL 280  
DB 1 EDKEDEEDVPGQAKDEL 19

## RESULT 2

US-08-045-261-9  
; Sequence 9, Application US/08045261  
; Patent No. 5426097  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Kuwabara, Keisuke  
; APPLICANT: Ryan, Jane  
; APPLICANT: Benedict, Claude  
; TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White - Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10112

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/045.261  
; FILING DATE: 19930406  
; CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; TELEX: 422523 COOPUT

## INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-045-261-9

Query Match 6.1%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.3e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 SGTIEDNPLITNDEAVA 202  
DB 1 SGTIEDNPLITNDEAVA 17

## RESULT 3

US-08-675-816-2  
; Sequence 2, Application US/08675816  
; Patent No. 6171864  
; GENERAL INFORMATION:  
; APPLICANT: Coughlan, Sean J.  
; APPLICANT: Winfrey, Jr., Ron J.  
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 701 Fifth Ave. Suite 6300

CITY: Seattle  
STATE: Washington

COUNTRY: U.S.A.

ZIP: 98104-7092

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675.816  
; FILING DATE: 05-JUL-1996

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6171864tendburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 750027.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)-622-4900  
; TELEFAX: (206)-682-6031

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-675-816-2

Query Match 4.6%; Score 13; DB 4; Length 415;  
Best Local Similarity 100.0%; Pred. No. 9.6e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 IPDDAKKPEDMD 117  
DB 244 IPDDAKKPEDMD 256

## RESULT 4

US-08-675-816-6  
; Sequence 6, Application US/08675816  
; Patent No. 6171864  
; GENERAL INFORMATION:  
; APPLICANT: Coughlan, Sean J.  
; APPLICANT: Winfrey, Jr., Ron J.  
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 701 Fifth Ave. Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675.816  
; FILING DATE: 05-JUL-1996  
; CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6171864tendburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 750027.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)-622-4900  
; TELEFAX: (206)-682-6031  
; INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
; LENGTH: 542 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-675-816-6

Query Match 3.9%; Score 11; DB 4; Length 542;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 KPEDMDERAKI 88  
|||||  
DB 234 KPEDMDERAKI 244

## RESULT 5

US-08-335-198-9  
Sequence 9, Application US/08335198  
Patent No. 5637454  
GENERAL INFORMATION:  
APPLICANT: Harley, John B.  
TITLE OF INVENTION: Assays and Treatments for Autoimmune  
TITLE OF INVENTION: Diseases  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Ste. 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309-4539  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,198  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/648205  
FILING DATE: 01-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Padst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF 114CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-335-198-9

Query Match 3.6%; Score 10; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.0041;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 QIDNPDYKGT 151  
|||||  
DB 8 QIDNPDYKGT 17

RESULT 6  
US-08-741-134-2

Sequence 2, Application US/08741134  
Patent No. 5861498

GENERAL INFORMATION:  
APPLICANT: Litwack, Gerald  
APPLICANT: Alnemrl, Emad S.  
APPLICANT: Fernandes-Alnemrl, Teresa  
TITLE OF INVENTION: IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING  
TITLE OF INVENTION: AND  
TITLE OF INVENTION: METHODS OF USING THE SAME  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5861498rls  
STREET: One Liberty Place - 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.11

SOFTWARE: WordPerfect for Windows 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/741,134

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/007,163

FILING DATE: 01-NOV-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TUV-2090

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 412 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-741-134-2

Query Match 3.2%; Score 9; DB 2; Length 412;  
Best Local Similarity 100.0%; Pred. No. 0.74;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDERDED 263  
|||||  
DB 198 DEDERDED 206

## RESULT 7

US-08-723-415B-4  
Sequence 4, Application US/08723415B  
Patent No. 5859199  
GENERAL INFORMATION:  
APPLICANT: Lathangue, Nicholas B.  
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NO. 5859199th Glebe Rd. 8th floor  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201-4741  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,415B  
FILING DATE: 30-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610195.1  
FILING DATE: 15-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Crawford, Arthur R.  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 117-220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 369 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-723-415B-4

Query Match 2.9%; Score 8; DB 2; Length 369;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262  
DB 355 DEDEDEE 362

RESULT 8  
US-09-189-627A-4  
Sequence 4, Application US/09189627A  
Patent No. 6159691  
GENERAL INFORMATION:  
APPLICANT: de la Luna, Susana  
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF  
FILE REFERENCE: 620-54  
CURRENT APPLICATION NUMBER: US/09/189,627A  
CURRENT FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: 08/723,415  
PRIOR FILING DATE: 1996-09-30  
PRIOR APPLICATION NUMBER: GB 9610195  
PRIOR FILING DATE: 1996-05-15  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 4  
LENGTH: 369  
TYPE: PRT  
ORGANISM: mouse  
US-09-189-627A-4

Query Match 2.9%; Score 8; DB 4; Length 369;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262  
DB 355 DEDEDEE 362

RESULT 9  
US-09-710-861-4  
Sequence 4, Application US/09710861  
Patent No. 6387649  
GENERAL INFORMATION:  
APPLICANT: La Thangue, Nicholas  
APPLICANT: de la Luna, Susana

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF  
FILE REFERENCE: 620-54  
CURRENT APPLICATION NUMBER: US/09/710,861  
CURRENT FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: US/09/189,627  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: 08/723,415  
PRIOR FILING DATE: 1996-09-30  
PRIOR APPLICATION NUMBER: GB 9610195  
PRIOR FILING DATE: 1996-05-15  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 4  
LENGTH: 369  
TYPE: PRT  
ORGANISM: mouse  
US-09-710-861-4

Query Match 2.9%; Score 8; DB 4; Length 369;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262  
DB 355 DEDEDEE 362

RESULT 10  
US-08-723-415B-6  
Sequence 6, Application US/08723415B  
Patent No. 5859199  
GENERAL INFORMATION:  
APPLICANT: LaThangue, Nicholas B.  
APPLICANT: de laLuna, Susana  
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 No. 5859199th GLebe Rd. 8th floor  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201-4741  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,415B  
FILING DATE: 30-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610195.1  
FILING DATE: 15-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Crawford, Arthur R.  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 117-220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 370 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-723-415B-6

Query Match 2.9%; Score 8; DB 2; Length 370;  
Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262  
| | | | | | | |  
Db 356 DEDEDEE 363

RESULT 11  
US-09-189-627A-6  
; Sequence 6, Application US/09189627A  
; Patent No. 6159691  
; GENERAL INFORMATION:  
; APPLICANT: La Thangue, Nicholas  
; APPLICANT: de la Luna, Susana  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF  
; FILE REFERENCE: 620-54  
; CURRENT APPLICATION NUMBER: US/09/189,627A  
; CURRENT FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 08/723,415  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: GB 9610195  
; PRIOR FILING DATE: 1996-05-15  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-189-627A-6

Query Match  
Best Local Similarity 100.0%; Score 8; DB 4; Length 370;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262  
| | | | | | | |  
Db 356 DEDEDEE 363

RESULT 12  
US-09-710-861-6  
; Sequence 6, Application US/09710861  
; Patent No. 6387649  
; GENERAL INFORMATION:  
; APPLICANT: La Thangue, Nicholas  
; APPLICANT: de la Luna, Susana  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF  
; FILE REFERENCE: 620-54  
; CURRENT APPLICATION NUMBER: US/09/710,861  
; CURRENT FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US/09/189,627  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 08/723,415  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: GB 9610195  
; PRIOR FILING DATE: 1996-05-15  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-710-861-6

Query Match  
Best Local Similarity 100.0%; Score 8; DB 4; Length 370;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262  
| | | | | | | |  
Db 356 DEDEDEE 363

RESULT 13  
US-08-723-415B-8  
; Sequence 8, Application US/08723415B  
; Patent No. 5859199  
; GENERAL INFORMATION:  
; APPLICANT: LaThangue, Nicholas B.  
; APPLICANT: delaluna, Susana  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 No. 5859199th Glebe Rd. 8th floor  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201-4741  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/723,415B  
; FILING DATE: 30-SEP-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9610195.1  
; FILING DATE: 15-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 117-220  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 385 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-723-415B-8

Query Match  
Best Local Similarity 100.0%; Score 8; DB 2; Length 385;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262  
| | | | | | | |  
Db 371 DEDEDEE 378

RESULT 14  
US-09-189-627A-8  
; Sequence 8, Application US/09189627A  
; Patent No. 6159691  
; GENERAL INFORMATION:  
; APPLICANT: La Thangue, Nicholas  
; APPLICANT: de la Luna, Susana  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF  
; FILE REFERENCE: 620-54  
; CURRENT APPLICATION NUMBER: US/09/189,627A  
; CURRENT FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 08/723,415  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: GB 9610195  
; PRIOR FILING DATE: 1996-05-15  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 385  
; TYPE: PRT

; ORGANISM: mouse  
US-09-189-627A-8

Query Match 2.9%; Score 8; DB 4; Length 385;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262  
|||||||  
DB 371 DEDEDEE 378

## RESULT 15

US-09-710-861-8  
; Sequence 8, Application US/09710861  
; Patent No. 6387649  
; GENERAL INFORMATION:  
; APPLICANT: La Thangue, Nicholas  
; APPLICANT: de la Luna, Susana  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF  
; FILE REFERENCE: 620-54  
; CURRENT APPLICATION NUMBER: US/09/710,861  
; CURRENT FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US/09/189,627  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 08/723,415  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: GB 9610195  
; PRIOR FILING DATE: 1996-05-15  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 385  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-710-861-8

Query Match 2.9%; Score 8; DB 4; Length 385;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262  
|||||||  
DB 371 DEDEDEE 378

Search completed: March 14, 2003, 20:50:11  
Job time : 16.7784 secs







FILE REFERENCE: 5051,503  
CURRENT APPLICATION NUMBER: US/09/844,006A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: 60/200,233  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Zea mays  
US-09-844-006A-2

Query Match 4.6%; Score 13; DB 10; Length 420;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 IPDPDAKKPEDMD 117  
Db 249 IPDPDAKKPEDMD 261

RESULT 7  
US-09-906-393A-6  
Sequence 6, Application US/09906393A  
Publication No. US20030039970A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Zhou  
APPLICANT: Xiao, Wuhan  
TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
FILE REFERENCE: 1720-1-001CIP  
CURRENT APPLICATION NUMBER: US/09/906,393A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 60/218,761  
PRIOR FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 12  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-906-393A-6

Query Match 4.3%; Score 12; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.9e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 INKDIRCKDDEF 31  
Db 1 INKDIRCKDDEF 12

RESULT 8  
US-09-906-393A-8  
Sequence 8, Application US/09906393A  
Publication No. US20030039970A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Zhou  
APPLICANT: Xiao, Wuhan  
TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
FILE REFERENCE: 1720-1-001CIP  
CURRENT APPLICATION NUMBER: US/09/906,393A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 60/218,761  
PRIOR FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 11  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-906-393A-8

Query Match 3.9%; Score 11; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00041;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 PTDSKPEDMDK 101  
Db 1 PTDSKPEDMDK 11

RESULT 9  
US-09-906-393A-9  
Sequence 9, Application US/09906393A  
Publication No. US20030039970A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Zhou  
APPLICANT: Xiao, Wuhan  
TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
FILE REFERENCE: 1720-1-001CIP  
CURRENT APPLICATION NUMBER: US/09/906,393A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 60/218,761  
PRIOR FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-906-393A-9

Query Match 3.9%; Score 11; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00041;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 PDARKPEDWDE 118  
Db 1 PDARKPEDWDE 11

RESULT 10  
US-09-745-763-115  
Sequence 115, Application US/09745763  
Patent No. US20020065394A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: Lavallie, Edward R.  
APPLICANT: Collins-Racie, Lisa A.  
APPLICANT: Evans, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM  
NUMBER OF SEQUENCES: 219  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/745,763  
FILING DATE: 18-Jun-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.

```

;
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-745-763-115

Query Match          3.2%; Score 9; DB 10; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEED 263
DB 615 DEDEDEED 623

RESULT 11
US-09-864-761-35241
; Sequence 35241, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35241
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL034548.24
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
US-09-864-761-35241

Query Match          2.9%; Score 8; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 KKRKEEE 244
DB 65 KKRKEEE 72

RESULT 12
US-09-864-761-35599
; Sequence 35599, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 33599  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AP000161.1  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2  
US-09-864-761-33599

Query Match  
Best Local Similarity 2.9%; Score 8; DB 10; Length 101;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 KKRKEEE 244  
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DB 61 KKRKEEE 68

RESULT 13  
US-09-864-761-36168  
Sequence 36168, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeonlca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 36168  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC011301.3  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 8.9  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 9.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 11  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.3  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8  
US-09-864-761-36168

Query Match  
Best Local Similarity 2.9%; Score 8; DB 10; Length 114;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDERDEE 262  
|||||||  
DB 65 DEDERDEE 72

RESULT 14  
US-09-844-006A-8  
Sequence 8, Application US/09844006A  
Patent No. US20020083496A1  
GENERAL INFORMATION:  
APPLICANT: Wyatt, Sarah  
APPLICANT: Robertson, Dominique  
APPLICANT: Boss, Wendy  
TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES  
FILE REFERENCE: 5051,503  
CURRENT APPLICATION NUMBER: US/09/844,006A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: 60/200,233  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Zea mays  
US-09-844-006A-8

Query Match  
Best Local Similarity 2.9%; Score 8; DB 10; Length 122;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 LMOVSGT 188  
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DB 27 LMOVSGT 34

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RESULT 15
US-09-925-300-1757
: Sequence 1757, Application US/09925300
: Patent No. US20020151681A1
: GENERAL INFORMATION:
: APPLICANT: Craig Rosen,
: APPLICANT: Steve Ruben
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA101
: CURRENT APPLICATION NUMBER: US/09/925,300
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05968
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1890
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1757
: LENGTH: 128
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (3)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (5)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (124)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (125)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (126)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (128)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1757

Query Match          2.9%; Score 8; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 EDEDEED 263
Db 106 EDEDEED 113

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Search completed: March 14, 2003, 20:51:13  
 Job time : 14.639 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 20.0573 Seconds  
(Without alignments)  
1342.037 Million cell updates/sec

Title: US-09-807-148-9  
Perfect score: 280  
Sequence: 1 GPGTKRVHVFNFYKGNVLI.....EDDKEDDEEDVPGQAKDEL 280

Scoring table: OLIGO  
Gapop 60.0 , Gapept 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280	100.0	417	1 A37047	calreticulin precu
2	165	58.9	418	1 A34154	calreticulin precu
3	88	31.4	416	1 S06763	calreticulin precu
4	88	31.4	416	2 JH0819	calreticulin precu
5	62	22.1	400	2 S43376	calreticulin, brai
6	55	19.6	421	2 S36799	calreticulin precu
7	39	13.9	411	2 S29129	calreticulin precu
8	23	8.2	336	2 A32507	41K larval antigen
9	22	7.9	384	2 S29130	calreticulin (clon
10	20	7.1	419	2 S71343	calreticulin precu
11	19	6.8	405	1 JH0795	calreticulin precu
12	17	6.1	395	2 S25851	calreticulin precu
13	16	5.7	406	2 A56637	calreticulin homol
14	14	5.0	393	1 A48573	calreticulin autoa
15	14	4.6	178	2 S26481	calcium-binding pr
16	13	4.6	415	2 T10172	calreticulin - cas
17	13	4.6	421	2 S58170	calreticulin precu
18	12	4.3	27	2 PC2299	calreticulin - Chi
19	11	3.9	389	2 T03691	calreticulin - com
20	11	3.9	412	2 T05703	calreticulin - bar
21	11	3.9	416	2 T05705	calreticulin - bar
22	11	3.9	415	2 T16968	calreticulin call
23	11	3.9	422	2 T07841	probable calreticu
24	11	3.9	428	2 T03251	calnexin - maize (
25	11	3.9	530	2 JN0597	calnexin-like prot
26	11	3.9	532	2 T49873	calnexin homolog -
27	11	3.9	540	2 T10892	probable calnexin
28	11	3.9	546	2 T06415	calnexin - soybean
29	9	3.2	77	2 AG2343	hypothetical prote

30	9	3.2	149	2 S39556	high mobility grou
31	9	3.2	361	2 S68268	apurinic/aprimidi
32	9	3.2	372	2 T04266	hypothetical prote
33	9	3.2	412	2 A55320	immunophilin FKBP4
34	9	3.2	425	2 C96605	calreticulin (CrtI
35	9	3.2	444	2 H86224	hypothetical prote
36	9	3.2	700	2 S38426	chaperonin 60 prec
37	9	3.2	712	2 JH0148	nucleolin - rat
38	9	3.2	798	2 T33022	hypothetical prote
39	8	2.9	190	2 T02015	hypothetical prote
40	8	2.9	207	2 B71446	hypothetical prote
41	8	2.9	215	1 S01947	nonhistone chromos
42	8	2.9	215	2 A28897	nonhistone chromos
43	8	2.9	215	2 S02826	nonhistone chromos
44	8	2.9	216	2 S29857	nonhistone chromos
45	8	2.9	260	2 G84714	hypothetical prote

## ALIGNMENTS

RESULT 1  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K Integrin-binding pr  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sonthelmer, R.D.; Capra, J.D.  
J: Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
A:Reference number: A42330; MUID:92129342; PMID:1733953  
A:Accession: A42330  
A:Molecule type: DNA  
A:Residues: 1-417 <MC2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:78536)  
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
J: Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
A:Reference number: A37047; MUID:90237213; PMID:2332496  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:Cross-references: GB:M42294; NID:9337486; PIDN:AAA36582.1; PID:9337487  
A:Note: the authors translated the codon GTA for residue 349 as Tyr  
R:Rokach, L.A.; Haselby, J.A.; Mellor, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.  
J: Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129; PMID:1919005  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:Cross-references: GB:M4739; NID:9179881; PIDN:AAA51916.1; PID:9179882  
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBI:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sonthelmer, R.D.  
J: Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence  
A:Reference number: A28812; MUID:88273610; PMID:3260607  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LRE>  
A:Note: 18-Ala was also found  
R:Dupuis, M.; Scherer, E.; Krause, K.H.; Tschopp, J.  
J: Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
A:Reference number: PH1525; MUID:93115648; PMID:8418194  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DUP>  
A:Experimental source: LAK cell  
R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

A:Reference number: A40346; MUID:92002034; PMID:1911778  
A:Accession: A40346  
A:Molecule type: protein  
A:Residues: 18-34; 'R' <ROOT>  
R:Krause, K.H.; Stimmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum retention signal  
A:Reference number: S11475; MUID:90380058; PMID:2400400  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRD>  
R:Ramirez, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.  
submitted to the EMBL data library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region  
A:Reference number: Z22906  
A:Accession: Z22906  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAMP>  
A:Cross-references: EMBL:AD000092; PIDN:AB51176.1  
A:Experimental source: cell line 5H12-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and C:Genetics:  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3  
A:Note: CRTC  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/bomains: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <ANT>  
F:414-417/Region: endoplasmic reticulum retention signal

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Best Local Similarity 100.0%; Pred. No. 2,5e-257;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVIENYKGNVNLINKDIRKDEFTHLTLIVRPDNTYEVKIDNSQVSGSLE 60  
Db 138 GPGTKKVVHVIENYKGNVNLINKDIRKDEFTHLTLIVRPDNTYEVKIDNSQVSGSLE 197  
QY 61 DDWDPLPKPKIKIDPDASKPEDMDERAKIDDPDSKPEDMDKPEHLPDDAKKPEDWDEM 120  
Db 198 DDWDPLPKPKIKIDPDASKPEDMDERAKIDDPDSKPEDMDKPEHLPDDAKKPEDWDEM 257  
QY 121 DGEWEPVYIQNPEYKGEKKPROINDPDYKGTWIMHEIDINPEKSPDSIYAYDNFGLGLD 180  
Db 258 DGEWEPVYIQNPEYKGEKKPROINDPDYKGTWIMHEIDINPEKSPDSIYAYDNFGLGLD 317  
QY 181 LMQVKSSTGFDFNFLTNDDEAVAEFGNETGWYTKAEKQMKDKODEQRLEKEEDKKRK 240  
Db 318 LMQVKSSTGFDFNFLTNDDEAVAEFGNETGWYTKAEKQMKDKODEQRLEKEEDKKRK 377  
QY 241 EEEEAEDKDEDEDKDE 280  
Db 378 EEEEAEDKDEDEDKDE 417

RESULT 2  
A34154  
calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34154; S13047  
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reitmeyer, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c  
A:Reference number: A34154; MUID:90094320; PMID:2600080  
A:Accession: A34154  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <FLD>

A:Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859  
 R:Cross-references: S: de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
 Biochem. J. 271, 473-480, 1990  
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
 A:Reference number: S13045; MUID:91054414; PMID:2241926  
 A:Accession: S13047  
 A:Molecule type: protein  
 A:Residues: 19-32 <TR>  
 C:Superfamily: calreticulin  
 C:Keywords: skeletal muscle  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 58.9%; Score 165; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. NO. 2.3e-148; Indels 0; Gaps 0;  
 Matches 165; Conservative 0; Mismatches 0;

1 GPGTKVAVINNYKGNVLINKDICKDEFTHTLTLVLRPDNTYEVKIDNSQVSGSLE 60  
 Db 138 GPGTKVAVINNYKGNVLINKDIRCKDEFTHTLTLVLRPDNTYEVKIDNSQVSGSLE 197  
 61 DDWDFLPKKIKIDPDASKPEDWDERAKIDDPDTSKPEDMDKPEHIDPDASKPEDWDEEM 120  
 Db 198 DDWDFLPKKIKIDPDASKPEDWDERAKIDDPDTSKPEDMDKPEHIDPDASKPEDWDEEM 257  
 Qy 121 DGEWPEPVIONPEYKGEWKPQIIONPDYKGVINHEIDNPEYSPD 165  
 Db 258 DGEWPEPVIONPEYKGEWKPQIIONPDYKGVINHEIDNPEYSPD 302

RESULT 3  
 506763  
 calreticulin precursor - mouse  
 N:Alternate names: 55k calcium-binding reticuloplasmic; calregulin  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S06763; JCI444; PCL233; A57498  
 R:Smith, M.J.; Koch, G.L.E.  
 E:EMBO J. 8, 3581-3586, 1989  
 A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a  
 A:Reference number: S06763; MUID:90059955; PMID:2583110  
 A:Accession: S06763  
 A:Molecule type: DNA  
 A:Residues: 1-416 <SM>  
 A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CA33053.1; PID:g50568  
 R:Marzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.  
 Gene 120, 217-225, 1992  
 A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/ca  
 A:Reference number: JCI444; MUID:99013037; PMID:1398135  
 A:Accession: JCI444  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <MZ>  
 A:Cross-references: GB:M2988; NID:g193084; PIDN:AAA37569.1; PID:g193085  
 A:Accession: PCL233  
 A:Molecule type: protein  
 A:Residues: 18-41 <MA>  
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.  
 J. Biol. Chem. 270, 15926-15929, 1995  
 A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mous  
 A:Reference number: A57498; MUID:9533280; PMID:7608143  
 A:Accession: A57498  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 74-80;142-151;186-193 <WH>  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-416/Product: calregulin #status experimental <MA>  
 F:413-416/Region: endoplasmic reticulum retention signal

Query Match 31.4%; Score 88; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. NO. 2.2e-75; Indels 0; Gaps 0;  
 Matches 88; Conservative 0; Mismatches 0;



QY 78 KPEDWDERAKIDPDTSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 137  
|||||  
Db 215 KPEDWDERAKIDPDTSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 274  
QY 138 WKPRQIDNDPYKGTWHPEDINPEYSPD 165  
|||||  
Db 275 WKPRQIDNDPYKGTWHPEDINPEYSPD 302

## RESULT 4

JH0819  
calreticulin precursor - rat  
N:Alternate names: calcium-binding protein 3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000  
C:Accession: JH0819; A49176; P01109; S45036; S04867; S39372; A34473; S13045  
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanohe, T.; Arai, K.; Okinaga, S.  
Exp. Cell Res. 205, 101-110, 1993  
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom  
A:Reference number: A49176; MUID:93202172; PMID:8453984  
A:Accession: JH0819  
A:Molecule type: mRNA  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572  
A:Accession: A49176  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-416 <NA2>  
A:Cross-references: NID:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572  
A:Experimental source: Sprague-Dawley, spermatogenic cells  
R:Murthy, K.K.; Banville, D.; Stikant, C.B.; Carlier, F.; Holmes, C.; Bell, A.; Patel, Y  
Nucleic Acids Res. 18, 4933, 1990  
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc  
A:Reference number: S11205; MUID:90370496; PMID:2395661  
A:Accession: S11205  
A:Molecule type: mRNA  
A:Residues: 1-416 <MUR>  
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855  
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.  
A:Reference number: P01109; MUID:92360010; PMID:1497655  
A:Accession: P01109  
A:Molecule type: protein  
A:Residues: 18-32 <NAK2>  
A:Experimental source: testis, strain Sprague-Dawley  
R:Soenichsen, B.; Funellekrug, J.; van Nuygen, P.; Diekmann, W.; Robinson, D.G.; Mieskes  
submitted to the EMBL Data Library, May 1994  
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul  
A:Reference number: S45036  
A:Accession: S45036  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <SOB>  
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA5890.1; PID:g488841  
R:Lone, Y.C.; Bailly, A.; Latriefe, N.  
submitted to the EMBL Data Library, December 1988  
A:Reference number: S04867  
A:Accession: S04867  
A:Molecule type: mRNA  
A:Residues: 'R', 270-358, 'AAG' <LON>  
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260  
A>Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R:Yohoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kametaki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an  
A:Reference number: S39371; MUID:94072621; PMID:8251535  
A:Accession: S39372  
A:Molecule type: protein  
A:Residues: 18-23, 'X', 25-32 <YOK>  
R:Van, P.N.; Peter, F.; Soelling, H.D.

J. Biol. Chem. 264, 17494-17501, 1989  
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes  
A:Reference number: A34473; MUID:90008920; PMID:2793869  
A:Accession: A34473  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-36 <VAN>  
R:Rieves, S.; de Matel, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414; PMID:2241926  
A:Accession: S13045  
A:Molecule type: protein  
A:Residues: 18-29 <RD>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-17/Domain: signal sequence #status predicted <Sig>  
F:18-416/Product: calreticulin #status experimental <Mat>  
F:204-212/Region: nuclear location signal  
F:413-416/Region: endoplasmic reticulum retention signal  
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.4%; Score 88; DB 2; Length 416;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-75;  
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 KPEDWDERAKIDPDTSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 137  
|||||  
Db 215 KPEDWDERAKIDPDTSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 274  
QY 138 WKPRQIDNDPYKGTWHPEDINPEYSPD 165  
|||||  
Db 275 WKPRQIDNDPYKGTWHPEDINPEYSPD 302

## RESULT 5

S43376  
calreticulin, brain isoform 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
C:Accession: S43376; S36801  
R:Matsumoto, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
Biochem. J. 298, 435-442, 1994  
A:Title: Covalent structure of bovine brain calreticulin.  
A:Reference number: S43376; MUID:94183174; PMID:8135753  
A:Accession: S43376  
A:Molecule type: protein  
A:Residues: 1-400 <MAT>  
A:Experimental source: brain  
R:Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticul  
A:Reference number: S36799; MUID:93385184; PMID:8373827  
A:Accession: S36801  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 45-63, 'E', 65-83 <LIU>  
A:Experimental source: brain, clone 8.1  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:397-400/Region: endoplasmic reticulum retention signal  
F:1120-1146/Disulfide bonds: #status experimental  
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 22.1%; Score 62; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 9, 1e-51;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 RAKIDPDTSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGEWKPRQID 144  
|||||  
Db 205 RAKIDPDTSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGEWKPRQID 264



F:19-419/Product: calreticulin #status predicted <MAT>  
F:205-213/Region: nuclear location signal  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 7.1%; Score 20; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 6e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLIVRPDNTYEYKIDN 52  
|||||  
Db 171 HLYTLIVRPDNTYEYKIDN 190

#### RESULT 11

JH0795 calreticulin precursor - California sea hare

C:Species: Aplysia californica (California sea hare)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: JH0795; B31409; F60977  
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.

A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin

A:Reference number: JH0795; MUID:93098937; PMID:1463604

A:Accession: JH0795

A:Molecule type: mRNA

A:Cross-references: GB:S51239; NID:g262053; PIDN:AA24569.1; PID:g262054

A:Experimental source: abdominal ganglion and antral nervous system

R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.

Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988

A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and

tion in Aplysia.

A:Reference number: A94207; MUID:88320566; PMID:3413132

A:Accession: B31409

A:Molecule type: Protein

A:Residues: 'X', 17-28, 'X', 30-31 <KE2>

R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.

Electrophoresis 10, 152-157, 1989

A:Title: Development of a database of amino acid sequences for proteins identified and

A:Reference number: A60977; MUID:89276264; PMID:2731514

A:Accession: F60977

A:Molecule type: Protein

A:Residues: 'X', 17-28, 'X', 30-31 <SME>

C:Superfamily: calreticulin

C:Keywords: calcium binding; endoplasmic reticulum

F:16-405/Product: signal sequence #status predicted <SIG>

F:402-405/Region: endoplasmic reticulum retention signal

Query Match 6.8%; Score 19; DB 1; Length 405;  
Best Local Similarity 100.0%; Pred. No. 5.1e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLIVRPDNTYEYKIDN 51  
|||||

Db 166 HLYTLIVRPDNTYEYKIDN 184

#### RESULT 12

S25851 calreticulin precursor - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999

C:Accession: S25851; T33996  
R:Smith, M.J.

DNA Seq. 2, 235-240, 1992

A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.

A:Reference number: S25851; MUID:9232978; PMID:1627827

A:Accession: S25851

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <SMT>

A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694

R:Bauer, C.; Courtney, L.; Laplant, Y.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid Y38A10A.

A:Accession: T33996

A:Reference number: Z21453

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-395 <BAU>

A:Cross-references: EMBL:AF125963; PIDN:AD14746.1; GSPDB:GN00023; CESP:Y38A10A.5

A:Experimental source: strain Bristol N2; clone Y38A10A

C:Genetics:

A:Gene: CESP:Y38A10A.5

A:Map position: 5

A:Introns: 107/3; 315/3

C:Superfamily: calreticulin

F:1-15/Domain: signal sequence #status predicted <SIG>

F:392-395/Region: endoplasmic reticulum retention signal

Query Match 6.1%; Score 17; DB 2; Length 395;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 KPEHIPPDPKRPEDWD 117  
|||||

Db 233 KPEHIPPDPKRPEDWD 249

RESULT 13  
A56637 calreticulin homolog precursor - fruit fly (Drosophila melanogaster)

N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog

C:Species: Drosophila melanogaster

C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999

C:Accession: A56637; A37158

R:Smith, M.J.

DNA Seq. 3, 247-250, 1992

A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticuli

A:Reference number: A56637; MUID:93208374; PMID:1296819

A:Accession: A56637

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-406 <SMT>

A:Cross-references: GB:X64461; NID:g7685; PIDN:CAA45791.1; PID:g7686

A>Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBI:P:128275)

R:McCaulliffe, D.P.; Zappl, E.; Lieu, T.S.; Michalak, M.; Southeimer, R.D.; Capra, J.D.

J. Clin. Invest. 86, 332-335, 1990

A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly h

A:Reference number: A37158; MUID:90307981; PMID:2365822

A:Accession: A37158

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>

C:Genetics:

A:Gene: FlyBase:Crc

A:Cross-references: FlyBase:FBgn0005585

A:Introns: 65/1; 222/3

C:Superfamily: calreticulin

C:Keywords: calcium binding; endoplasmic reticulum

F:1-17/Domain: signal sequence #status predicted <SIG>

F:403-406/Region: endoplasmic reticulum retention signal

Query Match 5.7%; Score 16; DB 2; Length 406;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEMDKPEHIPPDA 110  
|||||

Db 232 KPEMDKPEHIPPDA 247

#### RESULT 14

A48573

calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)  
C:Species: Schistosoma mansoni  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48573  
R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.  
Mol. Biochem. Parasitol. 57, 193-202, 1993  
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human  
A:Reference number: A48573; MUID:93165070; PMID:8433712  
A:Accession: A48573  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-393 <KHA>  
A:Cross-references: GB:M3097; NID:9160928  
A>Note: sequence inconsistent with the nucleotide translation  
A>Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBI:125086)  
C:Superfamily: calreticulin  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:390-393/Region: endoplasmic reticulum retention signal

## Query Match

5.0%; Score 14; DB 1; Length 393;

Best Local Similarity 100.0%; Pred. No. 2.7e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TKKVHYFNYKGN 17

DB 139 TKKVHYFNYKGN 152

## RESULT 15

S26481

calcium-binding protein, 57K - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C:Accession: S26481

R:Tuan, R.S.; Fitzpatrick, D.

submitted to the EMBL Data Library, September 1990

A:Description: Structural analysis of mouse placental 57-KD Calcium-binding protein.

A:Reference number: S26481

A:Accession: S26481

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-178 &lt;TUA&gt;

A:Cross-references: EMBL:X56603; NID:953597; PIDN:CAA39940.1; PID:953598

C:Keywords: calcium binding

## Query Match

4.6%; Score 13; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 RKEEAEADKEDD 251

DB 1 RKEEAEADKEDD 13

Search completed: March 14, 2003, 20:49:03  
Job time : 21.0573 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 10.6972 Seconds  
(without alignments)  
1085.643 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 280

Sequence: 1 GPGTKKVVHIFNVKGNVLI.....EEDKEDDEDVPGAKDEL 280

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	280	100.0	417	1 CRTG_HUMAN	P27797 homo sapien
2	165	58.9	418	1 CRTG_RABIT	P15253 oryctolagus
3	88	31.4	416	1 CRTG_MOUSE	P14211 mus musculu
4	88	31.4	416	1 CRTG_RAT	P18418 rattus norv
5	62	22.1	400	1 CRT1_BOVIN	P52133 bos taurus
6	55	19.6	421	1 CRT2_BOVIN	P42918 bos taurus
7	23	8.2	388	1 RAL1_ONCVO	P11012 onchocerca
8	17	6.1	395	1 CRTG_CABEL	P27798 caenorhabdl
9	16	5.7	406	1 CRTG_DROME	P29413 drosophila
10	14	5.0	393	1 CRTG_SCMA	O06814 drosophila
11	13	4.6	401	1 CRTG_EDGR	O92ny3 euglena gra
12	13	4.6	415	1 CRTG_RICCO	P93508 ricinus com
13	13	4.6	420	1 CRTG_MAIZE	O9SP22 zea mays (m
14	11	3.9	416	1 CRTG_NICPL	O40401 nicotiana p
15	11	3.9	421	1 CRTG_PRUAR	O9xf98 prunus arme
16	11	3.9	528	1 CAX2_ARATH	O38798 arabidopsis
17	11	3.9	530	1 CAX1_ARATH	P29402 arabidopsis
18	11	3.9	540	1 CALX_HELTU	O39914 helianthus
19	11	3.9	546	1 CALX_SOYBN	O39817 glycine max
20	11	3.9	551	1 CALX_PEA	O82709 pisum sativ
21	10	3.6	420	1 CRTG_CHIRE	O9st33 chlamydomon
22	10	3.6	424	1 CRTG_ORXSA	O9sl18 oryza sativ
23	9	3.2	149	1 HMGL_VICFA	P40620 vicia faba
24	9	3.2	361	1 APEA_DICDI	P51173 dictyostell
25	9	3.2	412	1 FKBA_SPOFR	O26466 spodoptera
26	9	3.2	424	1 CRT2_ARATH	O38858 arabidopsis
27	9	3.2	424	1 CRTG_DICDI	O23858 dictyostell
28	9	3.2	425	1 CRT1_ARATH	O04151 arabidopsis
29	9	3.2	700	1 CH60_PLAFC	P34940 plasmodium
30	9	3.2	712	1 NUCL_RAT	P13363 rattus norv
31	8	2.9	134	1 CLX2_NARJA	O42103 narke japon
32	8	2.9	191	1 RPOE_STRPY	P58053 streptococc
33	8	2.9	211	1 HMLX_HUMAN	O9ugv6 homo sapien

## ALIGNMENTS

RESULT 1	CRTG_HUMAN	STANDARD:	PRT:	417 AA.
AC	P27797;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60).			
GN	CALR OR CRTG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92013129; PubMed=1919005;			
RA	Rokeach L.A., Haselby J.A., Mellio J.F., Smeenk R.J., Unasch T.R.,			
RA	Greene B.M., Hoch S.O.;			
RT	"Characterization of the autoantigen calreticulin.";			
RT	J. Immunol. 147:3031-3039(1991).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90237213; PubMed=2332496;			
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,			
RA	Bechinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sonthelmer R.D.,			
RA	Capra J.D.;			
RT	"Molecular cloning, expression, and chromosome 19 localization of a			
RT	human Ro/SS-A autoantigen.";			
RT	J. Clin. Invest. 85:1379-1391(1990).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92129342; PubMed=1733953;			
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sonthelmer R.D., Capra J.D.;			
RT	"The 5'-flanking region of the human calreticulin gene shares			
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase			
RT	promoters.";			
RT	J. Biol. Chem. 267:2557-2562(1992).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RL	[5]			
RP	SEQUENCE FROM N.A.			
RA	Lamerding J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;			
RA	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Eye, Pancreas, and skin;			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE OF 18-36.			
RA	MEDLINE=92002034; PubMed=1911778;			
RA	Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;			
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A			
RT	antigen (calreticulin) with a highly conserved amino acid sequence in			

34	8	2.9	214	1 HMGI_BOVIN	P10103 bos taurus
35	8	2.9	214	1 HMGI_HUMAN	P09429 homo sapien
36	8	2.9	214	1 HMGI_PIG	P12682 sus scrofa
37	8	2.9	357	1 YML9_YEAST	O03208 saccharomyc
38	8	2.9	364	1 IE68_PRYKA	P24827 pseudorabie
39	8	2.9	377	1 PEKE_HUMAN	O75381 homo sapien
40	8	2.9	396	1 TRT_DROME	P19351 drosophila
41	8	2.9	416	1 CRTG_BERST	O92p01 berberis st
42	8	2.9	416	1 CRTG_BETVU	O81919 beta vulgar
43	8	2.9	424	1 CRT3_ARATH	O04153 arabidopsis
44	8	2.9	440	1 T2EA_MOUSE	O9d065 mus musculu
45	8	2.9	446	1 TDP2_MOUSE	O64163 mus musculu

RT the cytoplasmic domain of integrin alpha subunits.";  
 RL Biochemistry 30:9859-9866(1991).  
 RN (8)  
 RP SEQUENCE OF 18-32.  
 RX MEDLINE=90380058; PubMed=2400400;  
 RA Kriese K.H., Simerman H.K.B., Jones L.R., Campbell K.P.;  
 RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein  
 that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60  
 cells.";  
 RL Biochem. J. 270:545-548(1990).  
 RN (9)  
 RP SEQUENCE OF 18-28.  
 RC TISSUE=LIVER;  
 RX MEDLINE=93162045; PubMed=1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargass R.,  
 RA Appel R.D., Hughes G.J.;  
 RT "Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.";  
 RL Electrophoresis 13:992-1001(1992).  
 RN (10)  
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
 RC TISSUE=Keratinocytes;  
 RX MEDLINE=93162043; PubMed=1286667;  
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
 RA Vandekerckhove J.;  
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
 RT protein database of normal human epidermal keratinocytes.";  
 RL Electrophoresis 13:960-969(1992).  
 RN [11]  
 RP SEQUENCE OF 18-26.  
 RC TISSUE=Colon carcinoma;  
 RX MEDLINE=97293306; PubMed=9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
 RT "A two-dimensional gel database of human colon carcinoma proteins.";  
 RL Electrophoresis 18:605-613(1997).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro  
 CC autoantigen.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M84739; AAA51916.1; -;  
 DR EMBL; M32294; AAA36582.1; -;  
 DR EMBL; AY047586; AAL13126.1; -;  
 DR EMBL; AD000092; AAB51176.1; -;  
 DR EMBL; BC002500; AAH02500.1; -;  
 DR EMBL; BC007911; AAH07911.1; -;  
 DR EMBL; BC020493; AAH20493.1; -;  
 DR PIR; A37047; A37047.  
 DR PIR; S11475; S11475.  
 DR PIR; A42330; A42330.  
 DR PIR; A46452; A46452.  
 DR SWISS-2DPAGE; P27797; HUMAN.  
 DR Aarhus/Ghent-2DPAGE; 9401; IEF.  
 DR PMMA-2DPAGE; P27797; -;  
 DR PHCI-2DPAGE; P27797; -;  
 DR HSC-2DPAGE; P27797; HUMAN.  
 DR Sienna-2DPAGE; P27797; -;  
 DR Genev; HGNC:1455; CALR.  
 DR MIM; 109091; -;  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.

DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN; 1; 1.  
 DR PROSITE; PS00804; CALRETICULIN; 2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 417 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT SITE 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA: 48141 MW: 53730 Cys1054Fb2 CRC64;  
 Query Match 100.0%; Score 280; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-252;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTAKKVVHIVNYKGNVINKINDICKDETHLYTLVLPDNTYEKIDNSQVSGSIE 60  
 DB 138 GGTAKKVVHIVNYKGNVINKINDICKDETHLYTLVLPDNTYEKIDNSQVSGSIE 197  
 QY 61 DDMDFLPKKIKIDPPASKEPDMDERAKIDPPDSPEMDKREHIPPDPARKPEMDDEEM 120  
 DB 196 DDMDFLPKKIKIDPPASKEPDMDERAKIDPPDSPEMDKREHIPPDPARKPEMDDEEM 257  
 QY 121 DEWEPEPVQNPBYGKEMKROIINDPDYKGTWIHPEIDNPESPPSIYAYDNFGLGID 180  
 DB 256 DEWEPEPVQNPBYGKEMKROIINDPDYKGTWIHPEIDNPESPPSIYAYDNFGLGID 317  
 QY 181 LMQVSGTIFDNFLITNDEAVAEFNGETWGTAKAEKMKKODEORLKEEEDKKRK 240  
 DB 318 LMQVSGTIFDNFLITNDEAVAEFNGETWGTAKAEKMKKODEORLKEEEDKKRK 377  
 QY 241 EEEBAEDKEDDEDKDE 280  
 DB 378 EEEBAEDKEDDEDKDE 417  
 RESULT 2  
 CRTC\_RABIT  
 ID CRTC\_RABIT STANDARD; PRT; 418 AA.  
 AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HMCBP) (ERP60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Slow-twitch skeletal muscle;  
 RX MEDLINE=90094320; PubMed=2600080;  
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;  
 RT "Molecular cloning of the high affinity calcium-binding protein  
 (calreticulin) of skeletal muscle sarcoplasmic reticulum.";

RL J. Biol. Chem. 264:21522-21528(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fast-twitch skeletal muscle;  
 RX MEDLINE=91282795; PubMed=2059224;  
 RA Fliegel L., Michalak M.;  
 RT "Fast-twitch and slow-twitch skeletal muscles express the same  
 RT isoform of calreticulin.";  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 RN [3]  
 RP SEQUENCE OF 18-36.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Ianfredi M., Villa A., Green N.M.,  
 RA McLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [4]  
 RP SEQUENCE OF 18-46.  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum.";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=92002038; PubMed=1911780;  
 RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 RT monooxygenase and calreticulin.";  
 RL Biochemistry 30:9892-9900(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: J05138; AAA31188.1; -  
 DR PIR: A34154; A34154.  
 DR PIR: C33208; C33208.  
 DR PIR: D33208; D33208.  
 DR PIR: E33208; E33208.  
 DR PIR: F33208; F33208.  
 DR PIR: S13046; S13046.  
 DR PIR: S13047; S13047.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; Calreticulin.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 418 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 418 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.

FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 297 2-1.  
 FT REPEAT 259 297 2-2.  
 FT REPEAT 273 283 2-1.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 415 418 PREVENT SECRETION FROM ER.  
 FT VARIANT 35 35 E->D.  
 FT CONFLICT 90 90 P->T (IN REF. 5).  
 SQ SEQUENCE 418 AA; 48275 MW; B6082B68DC763A6 CAC64;  
 Query Match 58.9%; Score 165; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-146;  
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPGTKKAVIFNYKGNVINKDKDEDFHLYTLIVRPDNTYEVRKIDNSQVESGSL 60  
 DB 138 GPGTKKAVIFNYKGNVINKDKDEDFHLYTLIVRPDNTYEVRKIDNSQVESGSL 197  
 QY 61 DDWDFLPKRIKIDPDASKPEDWDERAKIDPTDSKPEDWDERKIDPDASKPEDWDEEM 120  
 DB 198 DDWDFLPKRIKIDPDASKPEDWDERAKIDPTDSKPEDWDERKIDPDASKPEDWDEEM 257  
 QY 121 DGEWPPYIQNPEYKGEKPPQIDNPDKGTWHPEDINPEKSPD 165  
 DB 258 DGEWPPYIQNPEYKGEKPPQIDNPDKGTWHPEDINPEKSPD 302  
 RESULT 3  
 CRIC\_MOUSE STANDARD; PRT; 416 AA.  
 AC CRIC\_MOUSE  
 ID P14211;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Calreticulin precursor (CRP55) (calregulin) (HACBP) (ERP60).  
 GN CALR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=90059955; PubMed=2583110;  
 RA Smith M.J., Koch G.L.E.;  
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,  
 RT HACBP), a major calcium binding ER/SR protein.";  
 RL EMBO J. 8:3581-3586(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93013037; PubMed=1398135;  
 RA Mazzerella R.A., Gold P., Cunningham M., Green M.;  
 RT "Determination of the sequence of an expressible cDNA clone encoding  
 RT Erp60/calregulin by the use of a novel nested set method.";  
 RL Gene 120:217-225(1992).  
 RN [3]  
 RP SEQUENCE OF 18-38.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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DR EMBL: X14926; CAA3053.1; -  
 DR EMBL: M92988; AAA37569.1; -  
 DR PIR: S06763; S06763.  
 DR PIR: J01444; J01444.  
 DR SWISS-2DPAGE: P14211; MOUSE.  
 DR MGD: MGI:88252; Calt.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin\_1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin\_1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 416 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 413 416 PREVENT SECRETION FROM ER.  
 FT SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CAC64;

Query Match 31.4%; Score 86; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 3e-74;  
 Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 KPEDDERAKIDDPDSKPEMDKPEHIPPDPARKPEMDDEMDGEMPEPVQNPYKGE 137  
 DB 215 KPEDDERAKIDDPDSKPEMDKPEHIPPDPARKPEMDDEMDGEMPEPVQNPYKGE 274

QY 138 WKPRQIDNPDKGTWVHPEIDNPESPD 165  
 DB 275 WKPRQIDNPDKGTWVHPEIDNPESPD 302

RESULT 4  
 CRIC\_RAT STANDARD: PRT; 416 AA.  
 AC P18418: P10452; (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 16, Last sequence update)  
 DT 01-NOV-1990 (Rel. 35, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (CALBP)  
 GN (Calcium-binding protein 3) (CABP3).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;

RX MEDLINE=90370496; PubMed=2395661;  
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,  
 RA Holmes C., Patel Y.C.;  
 RT "Structural homology between the rat calreticulin gene product and  
 RT the Oncoferrin volutus antigen Ral-1";  
 RL Nucleic Acids Res. 18:4933-4933(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=93202172; PubMed=8453984;  
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,  
 RA Okinaga S., Kobayashi T.;  
 RT "An endoplasmic reticulum protein, calreticulin, is transported into  
 RT the acrosome of rat sperm";  
 RL Exp. Cell Res. 205:101-110(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=95181573; PubMed=7876339;  
 RA Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Mieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain  
 RT calreticulin in the endoplasmic reticulum";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 RN [4]  
 RP SEQUENCE OF 270-358 FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Lone Y.C., Bailly A., Latruffe N.;  
 RL Submitted (DEC-1988) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 18-29.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA Macleannan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain";  
 RL Biochem. J. 271:473-480(1990).  
 RN [6]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
 RX MEDLINE=92360010; PubMed=1497655;  
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
 RT "Calreticulin is present in the acrosome of spermatids of rat  
 RT testis";  
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
 RN [7]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=LEC; TISSUE=Liver;  
 RX MEDLINE=94072621; PubMed=8251535;  
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
 RA Kanetaki T.;  
 RT "Identification of protein disulfide isomerase and calreticulin as  
 RT autoimmune antigens in LEC strain of rats";  
 RL Blochim. Biophys. Acta 1158:339-344(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-  
 CC HYDROXYBUTYRATE DEHYDROGENASE.  
 CC -----

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CC -----

DR EMBL: D78308; BAA11345.1; -  
 DR EMBL: X53363; CAA37446.1; -  
 DR EMBL: X13702; CAA31987.1; ALT\_SEQ.



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DR EMBL; X79327; CAAS5890.1; -
DR PIR; S04867; S04867.
DR PIR; S11205; S11205.
DR PIR; S13045; S13045.
DR PIR; A49176; A49176.
DR PIR; S45036; S45036.
DR PIR; JH0819; JH0819.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ERtarget.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 235 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;

Query Match 31.4%; Score 88; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 KPEWDERAKIDPTDSKPEWMDKREHIPPDAKKPEWDEMDGEWEPVYQNPYKGEK 137
Db 215 KPEWDERAKIDPTDSKPEWMDKREHIPPDAKKPEWDEMDGEWEPVYQNPYKGEK 274

Qy 138 WKPRQIDNPDKGTWHPHPEIDNPESPD 165
Db 275 WKPRQIDNPDKGTWHPHPEIDNPESPD 302

RESULT 5
CRT1_BOVIN
ID CRT1_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RL MEDLINE=94183174; PubMed=8135753;
RA Matsunaka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
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CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ERtarget.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.
FT DOMAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT REPEAT 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146
FT CARBOHYD 162 162
FT SITE 397 400 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 400 AA; 46381 MW; 7D4B6BDFC895EEF1 CRC64;

Query Match 22.1%; Score 62; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 RAKIDPDSKPEWMDKREHIPPDAKKPEWDEMDGEWEPVYQNPYKGEKRPD 144
Db 205 RAKIDPDSKPEWMDKREHIPPDAKKPEWDEMDGEWEPVYQNPYKGEKRPD 264

Qy 145 NP 146
Db 265 NP 266

RESULT 6
CRT2_BOVIN
ID CRT2_BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RL MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC EMBL: L13462; AAC37307.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin.1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; Calreticulin.1.  
DR PROSITE: PS00014; ER\_TARGET.1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
FT SIGNAL 1 34  
FT CHAIN 35 421  
FT DOMAIN 35 201 N-DOMAIN.  
FT DOMAIN 202 312 P-DOMAIN.  
FT DOMAIN 313 421 C-DOMAIN.  
FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.  
FT REPEAT 195 206 1-1.  
FT REPEAT 214 225 1-2.  
FT REPEAT 231 242 1-3.  
FT REPEAT 248 259 1-4.  
FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.  
FT REPEAT 263 273 2-1.  
FT REPEAT 277 287 2-2.  
FT REPEAT 291 301 2-3.  
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.  
FT DISULFID 141 167 BY SIMILARITY.  
FT CARBOHD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SITE 418 421 PREVENT SECRETION FROM ER.  
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 19.6%; Score 55; DB 1; Length 421;  
Best Local Similarity 100.0%; Pred. No. 1.4e-43;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 VLGLDLMOVKSGTIFDNLITNDENAYAEFEFGNETGVTKAEKQKDKODEQRL 230  
DB 317 VLGLDLMOVKSGTIFDNLITNDENAYAEFEFGNETGVTKAEKQKDKODEQRL 371

RESULT 7  
RAL1\_ONCVO STANDARD: PRT; 388 AA.  
ID RAL1\_ONCVO  
AC P11012;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE RAL-1 protein precursor (41 kDa larval antigen).  
GN RAL1.  
OS Onchocerca volvulus.  
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
CC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94341871; PubMed=7520419;  
RA Rokeach L.A., Zimmerman P.A., Unasch T.R.;  
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the  
RT calreticulin family of proteins, recognized by sera from patients  
RT with onchocerciasis.";  
RL Infect. Immun. 62:3696-3704(1994).  
RN [2]  
RP SEQUENCE OF 53-388 FROM N.A.  
RX MEDLINE=88273584; PubMed=2455736;  
RA Unasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;  
RT "Isolation and characterization of expression cDNA clones encoding  
RT antigens of Onchocerca volvulus infective larvae.";  
RL J. Clin. Invest. 82:262-269(1988).  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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CC EMBL: M20565; AAA59056.1; -  
DR PIR: A32507; A32507.  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin.1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; Calreticulin.1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
KW Calcium-binding; Repeat; Antigen; signal.  
FT SIGNAL 1 17  
FT CHAIN 18 388  
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
FT REPEAT 189 200 1-1.  
FT REPEAT 208 219 1-2.  
FT REPEAT 225 236 1-3.  
FT REPEAT 242 253 1-4.  
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
FT REPEAT 257 267 2-1.  
FT REPEAT 271 281 2-2.  
FT REPEAT 285 295 2-3.  
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
FT DISULFID 135 161 BY SIMILARITY.  
SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 8.2%; Score 23; DB 1; Length 388;  
Best Local Similarity 100.0%; Pred. No. 7e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 KPEDWDKEPHIPDPAPKPEDWD 117  
DB 230 KPEDWDKEPHIPDPAPKPEDWD 252

RESULT 8  
CRIC\_CAEEL STANDARD: PRT; 395 AA.  
ID CRIC\_CAEEL  
AC P27798;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Calreticulin precursor.  
GN CRT-1 OR Y38A10A.5.  
OS Caenorhabditis elegans.  
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
CC Rhabditidae; Peloderae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=92329978; PubMed=1627827;  
RA Smith M.J.;  
RT "A C. elegans gene encodes a protein homologous to mammalian  
RT calreticulin.";  
RL DNA Seq. 2:235-240(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX Bauer C., Courtney L., Laplant Y.;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP REVISIONS.  
RA Waterson R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL; X59589; CAA42159.1; -  
 DR EMBL; AF125963; AAD14746.1; -  
 DR PIR; S25851; S25851.  
 DR WormPep; Y38A10A.5; CE21562.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 15  
 FT CHAIN 16 395  
 FT DOMAIN ? 192  
 FT DOMAIN 193 301  
 FT DOMAIN 302 395  
 FT DOMAIN 186 250  
 FT REPEAT 186 197  
 FT REPEAT 205 216  
 FT REPEAT 222 233  
 FT REPEAT 239 250  
 FT DOMAIN 254 292  
 FT REPEAT 254 264  
 FT REPEAT 268 278  
 FT REPEAT 282 292  
 FT DOMAIN 332 390  
 FT DISULFID 133 158  
 FT SITE 392 395  
 FT SEQUENCE 395 AA: 45616 MW: 35CA/D2EC1D56B03 CRC64.  
 SQ  
 Query Match 6.1%; Score 17; DB 1; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a  
 RT calreticulin homologue";  
 RL DNA Seq. 3:247-250(1992).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktiroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paolel J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RN SEQUENCE OF 91-124 AND 182-220.  
 RP MEDLINE=90307981; PubMed=2365822;  
 RX McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sonthamer R.D.,  
 RA Capra J.D.;  
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
 RT highly homologous with oncohercal RAL-1 antigen and an aplysia  
 RT 'memory molecule'";  
 RL J. Clin. Invest. 86:332-335(1990).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 DR EMBL; X64461; CAA45791.1; -  
 DR EMBL; AE003683; AAF54416.1; -  
 DR PIR; A37158; A37158.  
 DR FlyBase; FBgn0005585; Crc.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.

DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 KM SIGNAL 1 17  
 FT CHAIN 18 406  
 FT CONFLICT 107 107 G -> A (IN REF. 3).  
 FT CONFLICT 184 184 V -> L (IN REF. 3).  
 SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;  
 Query Match 5.7%; Score 16; DB 1; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 95 KPEDMDKPEHIDPPDA 110  
 DB 232 KPEDMDKPEHIDPPDA 247  
 RESULT 10  
 CRIC\_SCHMA STANDARD; PRT; 393 AA.  
 AC 006814; Q26562;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Calreticulin precursor (SM4 protein).  
 OS Schistosoma mansoni (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;  
 OC Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Puerto Rican;  
 RX MEDLINE=93165070; PubMed=8433712;  
 RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,  
 RA Capron A.;  
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen  
 RT homologous to human Ro/SS-A autoantigen";  
 RL Mol. Biochem. Parasitol. 57:193-202(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Puerto Rican;  
 RX MEDLINE=94187805; PubMed=8139623;  
 RA Khalife J., Pierce R.J., Godin C., Capron A.;  
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni  
 RT calreticulin";  
 RL Mol. Biochem. Parasitol. 62:313-315(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL: M93097; AAA29854.1; -;  
 DR EMBL: L24159; AAA19024.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; Calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.

DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 KM SIGNAL 1 16  
 FT CHAIN 17 393  
 FT DOMAIN 189 254  
 FT REPEAT 189 200  
 FT REPEAT 209 220  
 FT REPEAT 225 236  
 FT REPEAT 243 254  
 FT DOMAIN 257 295  
 FT REPEAT 257 267  
 FT REPEAT 271 281  
 FT REPEAT 285 295  
 FT CARBOHYD 27 27  
 FT DISULFID 135 161  
 FT SITE 390 393  
 FT CONFLICT 89 90 MY -> IL (IN REF. 2).  
 FT CONFLICT 188 207 MISSING (IN REF. 2).  
 FT CONFLICT 378 378 Y -> D (IN REF. 2).  
 SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;  
 Query Match 5.0%; Score 14; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TKKVHVFYNYKGN 17  
 DB 139 TKKVHVFYNYKGN 152  
 RESULT 11  
 CRIC\_EUGGR STANDARD; PRT; 401 AA.  
 AC 092NY3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 OS Euglena gracilis.  
 OC Eukaryota; Euklenozoa; Euglenida; Euglenales; Euglena.  
 OX NCBI\_TaxID=3039;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Navaziz L., Balda B., Martin W., Mariani P.;  
 RT "Evidence for conservation of a calcium homeostat component:  
 RT purification characterization and cloning of calreticulin from Euglena  
 RT gracilis";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Y09816; CAA70945.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; Calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; FALSE\_NEG.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 401 CALRETICULIN.  
FT SITE 398 401 PREVENT SECRETION FROM ER (POTENTIAL).  
SQ SEQUENCE 401 AA: 45910 MW: 0568074C16292674 CRC64;

Query Match 4.6%; Score 13; DB 1; Length 401;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 DLWQKSGTIFDN 192  
DB 314 DLWQKSGTIFDN 326

RESULT 12  
CRTC\_RICCO STANDARD; PRT; 415 AA.

AC P93508;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calreticulin precursor.  
OS Ricinus communis (Castor bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
OX NCBI\_Taxid=3988;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=97435975; Pubmed=9290642;  
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;  
RT Cloning and characterization of the calreticulin gene from Ricinus  
commonis L.;  
RL Plant Mol. Biol. 34:897-911(1997).

CC - FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC - LOW AFFINITY CALCIUM-BINDING SITES.

CC - SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.

CC - SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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CC -----  
EMBL: U74631; AAB71420.1; -;  
DR EMBL: U74630; AAB71419.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00014; ER\_TARGET; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal; glycoprotein.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 415 CALRETICULIN.  
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).  
SQ SEQUENCE 415 AA: 47522 MW: DD5F452E76CC7F8C CRC64;

Query Match 4.6%; Score 13; DB 1; Length 415;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 IPDPDAKPEDMD 117  
|||||

DB 244 IPDPDAKPEDMD 256

RESULT 13  
CRTC\_MAIZE STANDARD; PRT; 420 AA.

AC Q9SP22;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calreticulin precursor.

OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_Taxid=4577;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Wyatt W.E., Tsou P.-L., Robertson D.;  
RT "Effects of altered expression of the calcium-binding protein  
calreticulin in Arabidopsis thaliana."  
RL submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC - FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC - LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
CC - SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (by similarity).  
CC - SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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CC -----  
EMBL: AF190454; AAF01470.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00014; ER\_TARGET; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; FALSE NEG.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal; glycoprotein.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 420 CALRETICULIN.  
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).  
SQ SEQUENCE 420 AA: 47939 MW: E73B7F43E7494735 CRC64;

Query Match 4.6%; Score 13; DB 1; Length 420;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 IPDPDAKPEDMD 117  
DB 249 IPDPDAKPEDMD 261  
|||||

RESULT 14  
CRTC\_NICPL STANDARD; PRT; 416 AA.

AC Q40401;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calreticulin precursor.

OS Nicotiana glauca (Leadwort-leaved tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

CC  Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
CC  Asteridae: euasterids I: Solanales; Solanaceae; Nicotiana.
OX  NCBI_taxid=4092;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Borisjuk N., Borisjuk L., Adler K., Stalio L., Tewes A.,
RA  Mantelffel R.:
RT  "Differential expression of calreticulin during somatic and
RT  zygotic embryogenesis of Nicotiana glauca L.,"
RL  Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC  LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: Z71395; CAA95999.1; -.
DR  InterPro: IPR001580; Calreticulin.
DR  InterPro: IPR000886; ER_target.
DR  Pfam: PF00262; calreticulin; 1.
DR  PRINTS: PR00626; CALRETICULIN.
DR  PRODOM: PD001866; Calreticulin; 1.
DR  PROSITE: PS00803; CALRETICULIN_1; 1.
DR  PROSITE: PS00804; CALRETICULIN_2; 1.
DR  PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR  PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
KW  Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT  CHAIN 1 27 POTENTIAL.
FT  SIGNAL 1 27 CALRETICULIN.
FT  CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
SQ  SEQUENCE 416 AA; 47481 MW; 5026F3152B8828C0 CRC64;

Query Match 3.9%; Score 11; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 DPDAKPEDMD 117
    |||||
    253 DPDAKPEDMD 263

RESULT 15
CRTC_PRUAR STANDARD; PRT; 421 AA.
AC 09XK98;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Prunus americana (Apricot).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots; Rosidae;
OC eustosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_taxid=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bergeron; TISSUE=Mesocarp; and Endocarp;
RA Mbeugue-A-Mbeugue D., Fils-Lycaon B.R.;
RT "Molecular cloning and nucleotide sequence of a calreticulin from
RT apricot (Prunus americana cv. Bergeron).";
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).

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CC  -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AF134733; AAD32207.1; -.
DR  InterPro: IPR001580; Calreticulin.
DR  InterPro: IPR000886; ER_target.
DR  Pfam: PF00262; calreticulin; 1.
DR  PRINTS: PR00626; CALRETICULIN.
DR  PRODOM: PD001866; Calreticulin; 1.
DR  PROSITE: PS00803; CALRETICULIN_1; 1.
DR  PROSITE: PS00804; CALRETICULIN_2; 1.
DR  PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR  PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
KW  Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT  CHAIN 1 22 POTENTIAL.
FT  SIGNAL 1 22 CALRETICULIN.
FT  CARBOHYD 23 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ  SEQUENCE 421 AA; 48416 MW; 4F5F94CBA6C6690 CRC64;

Query Match 3.9%; Score 11; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 DPDAKPEDMD 117
    |||||
    250 DPDAKPEDMD 260

```

Search completed: March 14, 2003, 20:45:10  
 Job time : 11.6972 secs

GenCore version 5.1.4.P5\_4578  
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## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 37.4403 Seconds  
(without alignments)  
1540.938 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 280

Sequence: 1 GPGTKKHVHFNFYKGNVLL.....EDDKEDDEEDVPGAKDEL 280

Scoring table: OLIGO

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTRMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	22.1	417	6	Q8SQ53
2	39	13.9	411	13	Q91710
3	32	11.4	214	4	Q9UDG2
4	30	10.7	321	13	Q9USG0
5	23	8.2	375	5	Q18478
6	23	8.2	387	5	Q97372
7	22	7.9	343	13	Q91711
8	22	7.9	417	13	Q9PUC1
9	21	7.5	406	5	Q8WR36
10	20	7.1	419	13	Q98984
11	19	6.8	403	5	Q76961
12	19	6.8	405	5	Q26268
13	18	6.4	68	6	Q9TS71
14	18	6.4	421	5	Q9U650
15	17	6.1	318	13	Q9PFX7
16	17	6.1	397	5	Q8WPG8

17	17	6.1	410	5	Q16893	016893 amblyomma a
18	16	5.7	395	5	Q96722	Q96722 taenia soli
19	16	5.7	406	5	Q9U916	Q9U916 dirosophila
20	16	5.7	407	5	Q8T903	Q8T903 aedes aegypt
21	13	4.6	178	11	Q62041	Q62041 mus musculu
22	13	4.6	321	10	Q41799	Q41799 zea mays (m
23	13	4.6	415	5	Q8WRU9	Q8WRU9 meloidogyne
24	13	4.6	421	10	Q43712	Q43712 zea mays (m
25	12	4.3	350	5	Q26514	Q26514 schistosoma
26	12	4.3	396	5	Q45034	Q45034 schistosoma
27	12	4.3	559	5	Q9NG26	Q9NG26 tritrichomo
28	11	3.9	380	11	Q9D9Q6	Q9D9Q6 mus musculu
29	11	3.9	384	4	Q96LN3	Q96LN3 homo sapien
30	11	3.9	384	4	Q96LN3	Q96LN3 homo sapien
31	11	3.9	389	10	Q40567	Q40567 dictyostell
32	11	3.9	412	10	Q40040	Q40040 nicotiana t
33	11	3.9	415	10	Q40041	Q40041 hordeum vul
34	11	3.9	422	10	Q22502	Q22502 brassica na
35	11	3.9	428	10	Q41798	Q41798 zea mays (m
36	11	3.9	532	10	Q9LY26	Q9LY26 arabidopsis
37	10	3.6	536	5	Q95P35	Q95P35 dictyostell
38	10	3.6	774	11	Q8RIQ5	Q8RIQ5 mus musculu
39	10	3.6	775	11	Q9D6C5	Q9D6C5 mus musculu
40	10	3.6	775	11	Q9D680	Q9D680 mus musculu
41	9	3.2	77	16	Q8YP97	Q8YP97 anabena sp
42	9	3.2	119	10	Q94I90	Q94I90 atropa bell
43	9	3.2	212	13	Q91764	Q91764 xenopus lae
44	9	3.2	214	13	Q9P0K9	Q9P0K9 gallus gall
45	9	3.2	215	13	Q9YH06	Q9YH06 gallus gall

## ALIGNMENTS

RESULT 1  
ID Q8SQ53 PRELIMINARY: PRT: 417 AA.  
AC Q8SQ53:  
DT 01-JUN-2002 (TRENBLREL. 21, Created)  
DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)  
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
DE Calreticulin.  
GN CRR  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hossain M.A., Takuma K., Minakata H., Nakajima T.;  
RT "Bovine brain calreticulin."  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB067687; BAB6913.1; -  
SQ SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;

Query Match 22.1%; Score 62; DB 6; Length 417;  
Best Local Similarity 100.0%; Pred. No. 9.1e-53;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	85	RAKIDDPDSKPEMDKREHIPPDAKRPEDMDSEMPYQNEPVGEMKPRD 144
DB	222	RAKIDDPDSKPEMDKREHIPPDAKRPEDMDSEMPYQNEPVGEMKPRD 281
QY	145	NP 146
DB	282	NP 283
RESULT 2		
ID	Q91710	PRELIMINARY: PRT: 411 AA.
AC	Q91710:	

```
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS.
RA Treves S., Zorzato F., Pozzan T.;
RL Blochem. J. 0:0-0(0).
DR EMBL; X67597; CAA47866.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KM Signal.
FT NON_TER 1 1
FT SIGNAL <1 12 POTENTIAL.
FT CHAIN 13 411 CALRETICULIN.
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E0EBEFA CRC64;

Query Match 13.9%; Score 39; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KPEDMDSEMDGEMPEPVIONPEYKGEKMKPROIDNPDKYK 150
DB 244 KPEDMDSEMDGEMPEPVIONPEYKGEKMKPROIDNPDKYK 282

RESULT 3
QY 09UDG2 PRELIMINARY; PRT; 214 AA.
AC 09UDG2.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CALRETICULIN-CALCIUM binding protein (Fragments).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA "Houen G., Koch C.;
RT "Human placental calreticulin: purification, characterization and
RT association with other proteins.";
RL Acta Chem. Scand. 48:905-911(1994).
DR InterPro: IPR001580; Calreticulin.
DR ProDom: PD001866; Calreticulin; 1.
FT NON_TER 1 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 11.4%; Score 32; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 120 MDGEMPEPVIONPEYKGEKMKPROIDNPDKYK 151
DB 117 MDGEMPEPVIONPEYKGEKMKPROIDNPDKYK 148

RESULT 4
QY 09U5G0 PRELIMINARY; PRT; 321 AA.
AC 09U5G0.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Calreticulin (Fragment).
OS Euplatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eplatrelinae; Eplatreus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RL "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
genes.";
J. Mol. Evol. 49:728-735(1999).
DR EMBL; AB025323; BAA84476.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DF898D42E7AER CRC64;

Query Match 10.7%; Score 30; DB 13; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.1e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DMDKPEHIPDPAPKRPEDMDSEMDGEMPEP 127
DB 134 DMDKPEHIPDPAPKRPEDMDSEMDGEMPEP 163

RESULT 5
QY 018478 PRELIMINARY; PRT; 375 AA.
AC 018478.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Rat-1 protein (Fragment).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA Macleanan K., Hoffman W.H., Taylor D.W.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001621; CAA04877.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375 375
SQ SEQUENCE 375 AA; 43842 MW; 03F7642F8F7A5B8 CRC64;
```



Query Match 8.2%; Score 23; DB 5; Length 375;  
Best Local Similarity 100.0%; Pred. No. 2.9e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEMDKPEHIPPDPKKPEMD 117  
|||||  
Db 230 KPEMDKPEHIPPDPKKPEMD 252

RESULT 6  
097372 PRELIMINARY; PRT; 387 AA.

AC 097372;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Calreticulin precursor.  
OS Dicrofilaria immitis (Canine heartworm).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Dicrofilaria.  
OX NCBI\_TaxID=6287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99094497; PubMed=9879888;  
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.,  
RT "Molecular characterization of a calcium-binding protein from the  
RL filarial parasite Dicrofilaria immitis."  
RM Mol. Biochem. Parasitol. 97:69-79(1998).  
DR EMBL; AF052978; AA003405.1;  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 387 CALRETICULIN.  
FT SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 8.2%; Score 23; DB 5; Length 387;  
Best Local Similarity 100.0%; Pred. No. 3e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEMDKPEHIPPDPKKPEMD 117  
|||||  
Db 230 KPEMDKPEHIPPDPKKPEMD 252

RESULT 7  
091711 PRELIMINARY; PRT; 343 AA.

AC 091711;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodidae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CNS;  
RA Treves S., Zorzato F., Porzan T.;  
RT "Identification of calreticulin isoform in the CNS."  
RL Biochem. J. 0:0-0(0).  
DR EMBL; X67598; CAA47867.1;  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
FT NON\_TER 1 1  
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA3B91DE1 CRC64;

Query Match 7.9%; Score 22; DB 13; Length 343;  
Best Local Similarity 100.0%; Pred. No. 2.6e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 FTHLYTLIVRPNTYEKIDNS 52  
|||||  
Db 140 FTHLYTLIVRPNTYEKIDNS 161

RESULT 8  
09PUC1 PRELIMINARY; PRT; 417 AA.

AC 09PUC1;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin.  
GN CALR.  
OS Brachydanio rerio (zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20190113; PubMed=10660676;  
RA Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.;  
RT "Genes dependent on zebrafish cyclops function identified by AFlp  
RT differential gene expression screen."  
RL Genesis 26:86-97(2000).  
DR EMBL; AF195882; AAF13700.1;  
DR ZFIN; ZDB-GENE-000208-17; calr.  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER-target.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN.1  
SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match 7.9%; Score 22; DB 13; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.1e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 175 GVLGDLWQVSGTIFDNFLIT 196  
|||||  
Db 312 GVLGDLWQVSGTIFDNFLIT 333

RESULT 9  
08WR36 PRELIMINARY; PRT; 406 AA.

AC 08WR36;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Calreticulin.  
OS Anopheles gambiae (African malaria mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
OC Anophelinae.  
OX NCBI\_TaxID=7165;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;  
RT "Towards a catalog for genes and proteins from the salivary gland of  
RT the malaria vector, Anopheles gambiae."  
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF457551; AAL68781.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin.1.  
DR PRINTS: PD001866; Calreticulin.  
DR ProDom: PD001866; Calreticulin.1.  
DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN\_1.  
DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN\_1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; UNKNOWN\_3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9931F1 CRC64;

Query Match 7.5%; Score 21; DB 5; Length 406;  
Best Local Similarity 100.0%; Pred. No. 2.9e-12;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 VESGLEDMDWFLPPKIKDP 74  
DB 188 VESGLEDMDWFLPPKIKDP 208

RESULT 10

O98984 PRELIMINARY; PRT; 419 AA.  
AC O98984;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin.  
OS Rana rugosa (Fringled frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
OX NCBI\_Taxid=8410;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96234004; PubMed-8654561;  
RA Yamamoto S., Nakamura M.;  
RT "Calnexin: its molecular cloning and expression in the liver of the  
RT frog, Rana rugosa."  
RL FEBS Lett. 387:27-32(1996).  
RN [2]

RP SEQUENCE FROM N.A.  
RX MEDLINE-96387817; PubMed-8795287;  
RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;  
RT "Strong expression of the calreticulin gene in the liver of Rana  
RT rugosa tadpoles, but not adult frogs."  
RL J. Exp. Zool. 275:431-443(1996).  
DR EMBL: D78589; BAA11425.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin.1.  
DR PRINTS: PD001866; Calreticulin.  
DR ProDom: PD001866; Calreticulin.1.  
DR PROSITE: PS00803; CALRETICULIN.1; 1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 7.1%; Score 20; DB 13; Length 419;  
Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLVPRDNTYEVKIDS 52  
DB 171 HLYTLVPRDNTYEVKIDS 190

RESULT 11  
O76961 PRELIMINARY; PRT; 403 AA.  
AC O76961;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin precursor.  
GN CRT.  
OS Necator americanus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.  
OX NCBI\_Taxid=51031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pritchard D.I., Brown A., Kasper G., McElroy P., Loukas A., Hewitt C.,  
RA Berry C., Fulkrug R., Beck E.;  
RT "A hookworm allergen which strongly resembles calreticulin."  
RL Parasite Immunol. 20:0-0(0).  
DR EMBL: AJ006790; CA07254.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin.1.  
DR PRINTS: PD001866; Calreticulin.  
DR ProDom: PD001866; Calreticulin.1.  
DR PROSITE: PS00803; CALRETICULIN.1; 1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL 1 16 POTENTIAL.  
SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match 6.8%; Score 19; DB 5; Length 403;  
Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEDMDKPEHIPPDAKKP 113  
DB 228 KPEDMDKPEHIPPDAKKP 246

RESULT 12  
O26268 PRELIMINARY; PRT; 405 AA.  
AC O26268;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin.  
GN CALRETICULIN.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
OC Aplysiidae; Aplysia.  
OX NCBI\_Taxid=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-93098937; PubMed-1463604;  
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;  
RT "Long-term sensitization training in Aplysia leads to an increase in  
RT calreticulin, a major presynaptic calcium-binding protein."  
RL Neuron 9:1013-1024(1992).  
DR EMBL: S51239; AAB24569.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin.1.  
DR PRINTS: PD001866; Calreticulin.  
DR ProDom: PD001866; Calreticulin.1.  
DR PROSITE: PS00803; CALRETICULIN.1; 1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 405 AA; 46738 MW; 14CA201840D1D69 CRC64;

Query Match 6.8%; Score 19; DB 5; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTLVLRPNDTYEVKIDN 51  
 |||||  
 DB 166 HLYTLVLRPNDTYEVKIDN 184

## RESULT 13

Q9TS71 PRELIMINARY; PRT; 68 AA.

AC Q9TS71; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
 DE CALRETICULIN-RUBELLA virus RNA binding protein (Fragments).  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP MEDLINE=95108040; PubMed=7809119;  
 RA Singh N.K., Atreya C.D., Nakhasi H.L.;  
 RT "Identification of calreticulin as a rubella virus RNA binding  
 RT protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:12770-12774(1994).  
 FT NON\_TER 1 1  
 FT NON\_CONS 18 19  
 FT NON\_CONS 31 32  
 FT NON\_CONS 49 50  
 FT NON\_TER 68 68  
 SQ SEQUENCE 68 AA; 7789 MW; 23243C0B1B8C80C CRC64;

Query Match 6.4%; Score 18; DB 6; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 6e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GTIPDNFLITNDEAYAE 204  
 |||||  
 DB 51 GTIPDNFLITNDEAYAE 68

## RESULT 14

Q9U6S0 PRELIMINARY; PRT; 421 AA.

AC Q9U6S0; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE Calreticulin precursor.  
 GN CALRET.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinozoa; Echinozoa; Echinodermata; Echinozoa; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Susan J.M., Just M.L., Lennarz W.J.;  
 RT "Cloning and Characterization of Alphan Integrin and Calreticulin in  
 RT Embryos of the Sea Urchin.";  
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF17915; AD55725.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.

DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 421  
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 6.4%; Score 18; DB 5; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KDIRCKDDEFTHTLTLIV 39  
 |||||  
 DB 158 KDIRCKDDEFTHTLTLIV 175

## RESULT 15

Q9PTX7 PRELIMINARY; PRT; 318 AA.

AC Q9PTX7; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Calreticulin (Fragment).  
 OS Leishmania reissneri.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Leishneria.  
 OX NCBI\_TaxID=7753;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
 RT genes.";  
 RL J. Mol. Evol. 49:729-735(1999).  
 FT NON\_TER 1 1  
 FT NON\_CONS 18 19  
 FT NON\_CONS 31 32  
 FT NON\_CONS 49 50  
 FT NON\_TER 68 68  
 SQ SEQUENCE 318 AA; 36997 MW; C88102EA1C61506 CRC64;

Query Match 6.1%; Score 17; DB 13; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHIFNYKGN 17  
 |||||  
 DB 37 GPGTKKVVHIFNYKGN 53

Search completed: March 14, 2003, 20:47:40  
 Job time : 38.4403 secs

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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 47.6027 Seconds  
(without alignments)  
783.783 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 280

Sequence: 1 GPGRKRVHVFNYKGNVLI.....EDKKEDEEDVPGQANDEL 280

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
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14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*  
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17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	280	100.0	280	21	AA192355
2	280	100.0	400	21	AA192350
3	280	100.0	417	10	AA192276
4	280	100.0	417	20	AA190927
5	280	100.0	417	21	AA192349
6	280	100.0	417	23	AA192591
7	280	100.0	417	23	AA192712
8	280	100.0	417	23	AA192851
9	122	43.6	122	20	AA190924
10	107	38.2	401	18	AA191156

11	69	24.6	122	20	AA190925
12	69	24.6	122	20	AA190926
13	67	23.9	70	21	AA190458
14	60	21.4	60	21	AA192354
15	60	21.4	61	21	AA192352
16	60	21.4	180	21	AA192351
17	49	17.5	49	21	AA192353
18	24	8.6	57	21	AA192422
19	19	6.8	19	18	AA192491
20	17	6.1	403	17	AA1904171
21	16	5.7	85	17	AA1904170
22	15	5.7	406	22	AA1904414
23	15	5.4	15	19	AA1904561
24	15	5.4	336	12	AA1912312
25	13	4.6	13	23	AA191844
26	13	4.6	13	23	AA191845
27	13	4.6	13	23	AA191846
28	13	4.6	177	23	AA192414
29	13	4.6	415	22	AA1906341
30	13	4.6	415	22	AA1906343
31	13	4.6	420	23	AA1906356
32	12	4.3	12	23	AA191840
33	11	3.9	11	23	AA191842
34	11	3.9	11	23	AA191843
35	11	3.9	385	21	AA1932385
36	11	3.9	394	21	AA1904449
37	11	3.9	394	21	AA1926285
38	11	3.9	394	21	AA1926284
39	11	3.9	530	21	AA1926284
40	11	3.9	530	21	AA1926284
41	11	3.9	532	21	AA1904448
42	11	3.9	542	22	AA1906342
43	11	3.9	548	21	AA1904447
44	11	3.9	567	21	AA1904610
45	10	3.6	17	18	AA1924918

## ALIGNMENTS

RESULT 1	AA192355	standard: Protein; 280 AA.
ID	AA192355	
AC	AA192355	
DT	10-AUG-2000	(first entry)
DE	Recombinant delta-120 calreticulin.	
XX	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition; endothelial cell; anti-angiogenic; neuroprotective; antidiabetic; cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic; anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.	
OS	Homo sapiens.	
OS	Synthetic.	
PN	WO200020577-A1.	
PD	13-APR-2000.	
PF	05-OCT-1999;	99WO-US23240.
PR	06-OCT-1998;	98US-0103438.
PA	(US) US DEPT HEALTH & HUMAN SERVICES.	
PI	Tosato G, Pike SE, Yao L;	
DR	WPI, 2000-303767/26.	
XX	Inhibiting endothelial cell growth and angiogenesis using calreticulin,	

PT useful for suppressing tumor growth  
XX  
PS Claim 4; Page 86; 99pp; English.  
XX  
CC This sequence comprises recombinant human calreticulin (AA92350)  
CC missing the N-terminal 120 amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The  
CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 280 AA:  
Query Match 100.0%; Score 280; DB 21; Length 280;  
Best Local Similarity 100.0%; Pred. No. 8.9e-270;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTKVHVIFNFKGNVLINRDKDEFTLTYLTVRPDTEYVKIDNSQVESGSL 60  
1 GGGTKVHVIFNFKGNVLINRDKDEFTLTYLTVRPDTEYVKIDNSQVESGSL 60  
DB 1 GGGTKVHVIFNFKGNVLINRDKDEFTLTYLTVRPDTEYVKIDNSQVESGSL 60  
QY 61 DDMDFLPKKIKDPDASKEDWDERAKIDPTDSKPEDMDKEPHIDPPAKKPEDWDEEM 120  
61 DDMDFLPKKIKDPDASKEDWDERAKIDPTDSKPEDMDKEPHIDPPAKKPEDWDEEM 120  
DB 61 DDMDFLPKKIKDPDASKEDWDERAKIDPTDSKPEDMDKEPHIDPPAKKPEDWDEEM 120  
QY 121 DGEWEPVTONPEYKGEKPRQIDNPDYKGTWHPHIDPEYSPDSIAYDNFVGLGD 180  
121 DGEWEPVTONPEYKGEKPRQIDNPDYKGTWHPHIDPEYSPDSIAYDNFVGLGD 180  
DB 121 DGEWEPVTONPEYKGEKPRQIDNPDYKGTWHPHIDPEYSPDSIAYDNFVGLGD 180  
QY 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKDKODEQRKLEEDDKRR 240  
181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKDKODEQRKLEEDDKRR 240  
DB 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKDKODEQRKLEEDDKRR 240  
QY 241 EEEBAEDKEDDE 280  
241 EEEBAEDKEDDE 280  
DB 241 EEEBAEDKEDDE 280  
RESULT 2  
AA92350  
ID AA92350 standard; Protein; 400 AA.  
XX  
AC AA92350;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant human MBP-calreticulin.  
XX  
KM MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KM cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;  
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US23240.  
XX

PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX  
PI Tosato G, Pike SE, Yao L;  
XX  
DR WPI; 2000-303767/26.  
XX  
DR N-PSDB; AA09346, AA09347.  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
XX useful for suppressing tumor growth  
PS Claim 4; Page 80-81; 99pp; English.  
XX  
XX Recombinant human MBP-calreticulin comprises the sequence of human  
XX calreticulin (see AA92349) without the 17 N-terminal amino acids.  
XX A novel method of inhibiting endothelial cell growth comprises  
XX contacting the cells with calreticulin (or its fragments/variants).  
XX Fragments of calreticulin causes at least 40% inhibition of  
XX angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
XX method may be used for inhibiting angiogenesis in a patient. The  
XX angiogenesis is associated with a disease other than a tumor that is  
XX associated with neovascularization (e.g. diabetic neuropathy, retrolental  
XX fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
XX immune inflammation, atherosclerosis, excessive wound repair, retinal  
XX neovascularization, macular degeneration, corneal graft rejection,  
XX contact lens overwear, Crohn's disease, non-immune inflammation,  
XX rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
XX Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
XX syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
XX also be used for treating/inhibiting tumor growth especially  
XX Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 400 AA:  
Query Match 100.0%; Score 280; DB 21; Length 400;  
Best Local Similarity 100.0%; Pred. No. 1.2e-269;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPGTKVHVIFNFKGNVLINRDKDEFTLTYLTVRPDTEYVKIDNSQVESGSL 60  
1 GPGTKVHVIFNFKGNVLINRDKDEFTLTYLTVRPDTEYVKIDNSQVESGSL 60  
DB 1 GPGTKVHVIFNFKGNVLINRDKDEFTLTYLTVRPDTEYVKIDNSQVESGSL 60  
QY 121 DGEWEPVTONPEYKGEKPRQIDNPDYKGTWHPHIDPEYSPDSIAYDNFVGLGD 180  
121 DGEWEPVTONPEYKGEKPRQIDNPDYKGTWHPHIDPEYSPDSIAYDNFVGLGD 180  
DB 121 DGEWEPVTONPEYKGEKPRQIDNPDYKGTWHPHIDPEYSPDSIAYDNFVGLGD 180  
QY 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKDKODEQRKLEEDDKRR 240  
181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKDKODEQRKLEEDDKRR 240  
DB 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKDKODEQRKLEEDDKRR 240  
QY 241 EEEBAEDKEDDE 280  
241 EEEBAEDKEDDE 280  
DB 241 EEEBAEDKEDDE 280  
RESULT 3  
AAP92276  
ID AAP92276 standard; Protein; 417 AA.  
XX  
AC AAP92276;  
XX  
DT 23-FEB-1990 (first entry)  
XX  
DE 60 kD Ro (Ro/SSA) antigen.  
XX  
KM Sjorens syndrome; systemic lupus erythematosus.  
XX  
OS Synthetic.  
XX

XX	
PN	WO8909273-A.
XX	
PD	05-OCT-1989.
XX	
PF	22-MAR-1989; 69WO-US01213.
XX	
PR	22-MAR-1988; 88US-0171634.
XX	
PA	(TEXA ) UNIV OF TEXAS SYST.
XX	
PI	Sontheimer RD, Capra JD, McCauliffe DP;
XX	
DR	WPI; 1989-309537/42.
DR	N-PSDB; AAP92276.
XX	
PT	DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
PT	- used in immunoassays to detect rheumatic disease
XX	
PS	Disclosure; Fig 2; 88pp; English.
XX	
CC	Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC	expressed recombinantly to detect autoantibodies, for identification
CC	of autoimmune diseases. These epitopes are Aas 24-36, 23-36, 188-209,
CC	or 241-255. The peptides may be substd. for ribonucleoprotein particle
CC	antigens.
XX	
XQ	Sequence 417 AA;

Query Match	100.0%;	Score 280;	DB 10;	Length 417;
Best Local Similarity	100.0%;	Pred. No. 1.3e-269;		
Matches 280; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	GPRKXVAVIENYKGNVNLKDKIRCKDDDEETHLXYTLIVPDMNYEKKINDSQVESSSLE	60
Dp	138	GGGRKKAVIENYKGNVNLKDKIRCKDDDETHLYTLIVRDNMYEKKINDSQVESSSLE	197
Qy	61	DQMDFLPPEKKIKDPDASKPEDMWDERAKIDPDTDSKPEDMWDKPEHIIPDPDAKKPEDMQDEEM	120
Dp	198	DDMDFLPPEKKIKDPDASKPEDMWDERAKIDPDTDSKPEDMWKPPEHIIPDPDAKKPEDMQDEEM	257
Qy	121	DGEWPPYIQNPPEYKGEKKPQMDINPDYKGTWIIHPEIDNPESYSDPSITYADNFGVGLD	180
Dp	258	DGEWPPYIQNPPEYKGEKKPQMDINPDYKGTWIIHPEIDNPESYSDPSITYADNFGVGLD	317
Qy	181	LMQVKSQGITFENFLITNDDEAAEEFGNETWVTAKAEKOMKDKODEQRKLEEEEDKKRK	240
Dp	318	LMQVKSQGITFENFLITNDDEAAEEFGNETWVTAKAEKOMKDKODEQRKLEEEEDKKRK	377
Qy	241	EEBEAEDEKDEDEKDEBEDEDEKDEEDEDVPGQAKDEL	280
Dp	378	EEBEAEDEKDEDEKDEBEDEDEKDEEDEDVPGQAKDEL	417

RESULT 4	
AAV00927	
ID	AAV00927 standard; Protein; 417 AA

AC	AAy00927;
XX	
DT	28-MAY-1999 (first entry)
XX	
DE	Calreticulin.
XX	
KW	C1q and collectin receptor; C1qR binding domain; complement ubiquitin;
KW	C3b functionality; inhibitor; complement activation; inflammation;
KW	amyocardial infarction; brain ischemia; gut ischemia; amyloid plaque;
KW	rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW	immune complex nephritis; therapy.
XX	
OS	Homo sapiens.
XX	
PN	W09907406-A1.

XX 18-FEB-1999.  
PD  
XX  
XX 12-AUG-1996; 98MO-GB02430.  
PF  
XX  
PR 12-AUG-1997; 97GB-0016998.  
XX  
XX  
PA (UYLE-) UNIV LEICESTER.  
XX  
PI Schwaeble W;  
DR  
XX WPI; 1999-180404/15.  
XX  
PT  
PT use of a cC1qR binding domain - to modulate complement ubiquitin  
(CUB) functionality.  
PS  
PS Disclosure: Page 26-27; 31pp; English.

XX  
XX This sequence is calreticulin, a homologue of C1q and collectin receptor  
CC (cC1qR). The invention relates to the use of a cC1qR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB  
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
SQ Sequence 417 AA:

Query Match	100.0%;	Score 280;	DB 20;	Length 417;
Best Local Similarity	100.0%;	Pred. No. 1.3e-269;		
Matches 280;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	GGGTAKVAVIINYKGNLNLKOLRCADDETHLYTLVLRPNDTYEVKIDNSQVSSSLE	60
Db	138	GGGTAKVAVIINYKGNLNLKOLRCADDETHLYTLVLRPNDTYEVKIDNSQVSSSLE	197
Qy	61	DDMDLPEPKIKIDPDASKPEMDERAKIDDTDSKPEMDKPEHIIPPDAKKPEMDMEEM	120
Db	198	DDMDLPEPKIKIDPDASKPEMDERAKIDDTDSKPEMDKPEHIIPPDAKKPEMDMEEM	257
Qy	121	DGEMPPAIQNPYKGEKKPQOINDPYKGTWHPHETIDNPETYSDDPSITAYDNFGVGLD	180
Db	258	DGEMPPAIQNPYKGEKKPQOINDPYKGTWHPHETIDNPETYSDDPSITAYDNFGVGLD	317
Qy	181	LMQVSGTIFGNFLTINDNEAAAEFGNTEGWTVTAAEKOMKODKDEORLKEEEEDKKR	240
Db	318	LMQVSGTIFGNFLTINDNEAAAEFGNTEGWTVTAAEKOMKODKDEORLKEEEEDKKR	377
Qy	241	EEFEADKEDDEDDKDEDEEDKKEDEEDVPQOAKDEL	280
Db	378	EEFEADKEDDEDDKDEDEEDKKEDEEDVPQOAKDEL	417

RESULT 5  
AAV92349  
ID AAV92349 standard; Protein; 417 AA

AC	AAV92349;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Human MBP-calreticulin.
XX	
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition; endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW	cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

xx		AAE24591 standard; Protein; 417 AA.
ID	AAE24591	
AC	AAE24591;	
XX		
DT	04-OCT-2002 (first entry)	
XX		
DE	Human calreticulin protein.	
XX		
KW	Human; calreticulin; antisense compound; hyperproliferative disorder; cancer; autoimmune disease; viral infection; cardiovascular disease; antisense therapy; cytostatic; immunosuppressive; virucide.	
XX		
OS	Homo sapiens.	
PX	MO200236743-A2.	
PN		
PD	10-MAY-2002.	
XX		
PF	30-OCT-2001; 2001WO-US49045.	
XX		
PR	30-OCT-2000; 2000US-0702327.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Bennett CF, Cowsett LM;	
DR	WPI: 2002-479759/51.	
DR	N-PADB; AAD39469.	
PT	Noval antisense compound targeted to nucleic acid encoding calreticulin, useful for treating a human having disease or condition associated with calreticulin e.g. cancer, viral infection, autoimmune disease -	
PT		
PS	Disclosure; Page 88-90; 109pp; English.	
XX		
CC	The invention relates to antisense compounds, compositions comprise for modulating the expression of calreticulin. The compositions comprise antisense compounds, particularly antisense oligonucleotides, targeted to nucleic acids encoding calreticulin. The antisense compound is useful for inhibiting the expression of calreticulin in human cells or tissues. It is also useful for treating a human having a disease or condition associated with calreticulin, e.g., hyperproliferative disorder e.g., cancer, autoimmune disease, viral infection or cardiovascular disease, by inhibiting expression of calreticulin. It is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is also used in antisense therapy. The present sequence is human calreticulin protein. This sequence is used in the exemplification of the invention.	
XX		
SQ	Sequence 417 AA;	
Query Match	100.0%; Score 280; DB 23; Length 417;	
Best Local Similarity	100.0%; Pred. No. 1.3e-269;	
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 GGPGTKVAVINFYKKKNVLINKDKCKDPEFHLVTLYVRPNTYEVKINDSQVESGSL E 60	
Db	138 GGGIKKVVIVIFYKKKNVLINKDKCKDPEFHLVTLLYVRPNTYEVKINDSQVESGSLE 197	
OY	61 DDWFPLPKRIKDPPASRPEDMDERAKIDDPDSKPEDMCKREHLPDDPAKRPEDMDEEM 120	
Db	198 DDMDFLPPRKTIKDPDASKRPEDMDERAKIDDPDSKPEDMCKREHLPDDPAKRPEDMDEEM 257	
OY	121 DGEMEPPVIQNPEYKGEMKPROINDPDYKGTWIHPEDINPEXSPPDSPSYAYNFGVLGD 180	
Db	258 DGEMEPPVIQNPEYKGEMKPROINDPDYKGTWIHPEDINPEXSPPDSPSYAYNFGVLGD 317	
OY	181 LMOVKSGLIIFNFLTITNDGAFAEEEGNGTGWATKAEEKOMDKOQEORLKKEEEDDKRR 240	
Db	318 LMOVKSGLIIFNFLTITNDGAFAEEEGNGTGWATKAEEKOMDKOQEORLKKEEEDDKRR 377	



Db 258 DGEWEPV I Q N P E Y K G E W K P R Q I D N P D Y K G T W I H P E I D N P E Y S P D P S I Y A Y D N F G V L G L D 317

CC The invention further relates to a method of identifying a subject with

CC a slow growing form of prostate cancer. T1D-1 sequences are useful for  
CC treating cancers such as epithelium-derived carcinomas, kidney cancers,  
CC lymphomas, leukaemias and prostate cancers. Sequences of the invention  
CC are used as vaccines and in gene therapy. The present sequence is human  
CC calreticulin protein.

XX Sequence 417 AA;

Query Match 100.0%; Score 280; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-269;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKRVHYIFNYKKNVYLINDIRCKDDEFTHLTYLIVRPNTYEKVIDNSQVESGSL 60  
DB 138 GPGTKRVHYIFNYKKNVYLINDIRCKDDEFTHLTYLIVRPNTYEKVIDNSQVESGSL 197  
QY 61 DDMDFLPKKIKDPASKPEMDERAKIDDPDTSKPEMDKREHIPPDPARKPEMDDEEM 120  
DB 198 DDMDFLPKKIKDPASKPEMDERAKIDDPDTSKPEMDKREHIPPDPARKPEMDDEEM 257  
QY 121 DGEWEPVYIONPEYKGEWKPRQIDNPDKGTWVHPEIDNPESPPSIVAYDNFVGLGD 180  
DB 258 DGEWEPVYIONPEYKGEWKPRQIDNPDKGTWVHPEIDNPESPPSIVAYDNFVGLGD 317  
QY 181 LMQVSSGITFDNFLTINDEAVAEFGNETGWYTKAAEKOMKRODEORLKEEEDKKRK 240  
DB 318 LMQVSSGITFDNFLTINDEAVAEFGNETGWYTKAAEKOMKRODEORLKEEEDKKRK 377  
QY 241 EEEEADEKDEDDKDE 280  
DB 378 EEEEADEKDEDDKDE 417

RESULT 9

AAV00924  
ID AAV00924 standard; Protein; 122 AA.

AC AAV00924;

DT 28-MAY-1999 (first entry)

XX Human cClqR binding domain protein sequence.

DE Human cClqR binding domain protein sequence.  
KW C1q and collectin receptor; cClqR binding domain; complement ubiquitin;  
KW CUB functional activity; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.

XX Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI; 1999-180404/15.

XX N-PSDB; AAX27251.

XX Use of a cClqR binding domain - to modulate complement ubiquitin

XX Claim 9; Page 23; 31pp; English.

XX This sequence is a C1q and collectin receptor (cClqR) binding  
CC domain. The invention relates to the use of a cClqR binding domain in a

CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.

XX Sequence 122 AA;

Query Match 43.6%; Score 122; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.9e-113;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RCKDDEFTHLTYLIVRPNTYEKVIDNSQVESGSLDDMDFLPPKKIKDPASKPEMD 84  
DB 1 RCKDDEFTHLTYLIVRPNTYEKVIDNSQVESGSLDDMDFLPPKKIKDPASKPEMD 60  
QY 85 RAKIDPPTDSKPEMDKREHIPPDPARKPEMDDEEMDGEWEPVYIONPEYKGEWKPRQID 144  
DB 61 RAKIDPPTDSKPEMDKREHIPPDPARKPEMDDEEMDGEWEPVYIONPEYKGEWKPRQID 120  
QY 145 NP 146  
DB 121 NP 122

RESULT 10

AAW11156  
ID AAW11156 standard; peptide; 401 AA.

AC AAW11156;

DT 31-MAY-1997 (first entry)

XX Calreticulin.

XX calreticulin; C-domain; restenosis; inhibitor.

XX Homo sapiens.

XX WO9636643-A1.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-1B00471.

XX 16-MAY-1996; 96US-0649417.

XX 17-MAY-1995; 95US-0442844.

XX (UYAL-) UNIV ALBERTA.

XX Lucas A, Michalak M;

XX WPI; 1997-012036/01.

XX Inhibition of restenosis in patients - using calreticulin or a  
PT C-domain polypeptide of calreticulin or a variant with the same  
PT activity.

XX Disclosure; Fig 1; 48pp; English.

XX The present sequence is calreticulin. It and a C-domain derived peptide  
CC (AAW06736) are useful for treating a patient to inhibit restenosis. The  
CC calreticulin-type cpds. are administered either parenterally,  
CC intravenously or via a catheter and can target areas of vascular damage  
CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

Query Match 38.2%; Score 107; DB 18; Length 401;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHIFNFKGNVLIINKIRCKDEFTHTLVIRPDNTYEVRINDSQVESGSL 60  
DB 121 GPGTKKVVHIFNFKGNVLIINKIRCKDEFTHTLVIRPDNTYEVRINDSQVESGSL 180

QY 61 DDWDFLPKKIKDPDASKPEMDKREHIIPD 107  
DB 181 DDWDFLPKKIKDPDASKPEMDKREHIIPD 227

RESULT 11  
ID AAY00925 standard; Protein: 122 AA.  
AC AAY00925;  
XX  
XX 28-MAY-1999 (first entry)  
DE Mouse cC1qR binding domain protein sequence.  
XX  
XX C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
XX Mus musculus.  
OS  
XX MO9907406-A1.  
PN  
XX 18-FEB-1999.  
PD  
XX 12-AUG-1998; 98WO-GB02430.  
PF  
XX 12-AUG-1997; 97GB-0016998.  
PR  
XX (UYLE-) UNIV LEICESTER.  
PA  
XX Schaeble W;  
PI  
XX WPI: 1999-180404/15.  
DR N-PSDB: AAX27252.  
DR  
XX  
XX Use of a cC1qR binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
XX  
XX Claim 9; Page 24; 31pp; English.  
PS  
XX This sequence is a C1q and collectin receptor (cC1qR) binding  
CC domain. The invention relates to the use of a cC1qR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB  
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
XX Sequence 122 AA;  
SQ

Query Match 24.6%; Score 69; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.7e-60;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 KPEMDERAKIDDPDTSKPEMDKREHIIPDPAKKPEMDDEMDGEMPEPVIONPEYKGE 137

DB 54 KPEMDERAKIDDPDTSKPEMDKREHIIPDPAKKPEMDDEMDGEMPEPVIONPEYKGE 113  
OY 138 WKPROIDNP 146  
DB 114 WKPROIDNP 122

RESULT 12  
ID AAY00926 standard; Protein: 122 AA.  
AC AAY00926;  
XX  
XX 28-MAY-1999 (first entry)  
DE Rat cC1qR binding domain protein sequence.  
XX  
XX C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
XX Rattus norvegicus.  
OS  
XX MO9907406-A1.  
PN  
XX 18-FEB-1999.  
PD  
XX 12-AUG-1998; 98WO-GB02430.  
PF  
XX 12-AUG-1997; 97GB-0016998.  
PR  
XX (UYLE-) UNIV LEICESTER.  
PA  
XX Schaeble W;  
PI  
XX WPI: 1999-180404/15.  
DR N-PSDB: AAX27253.  
DR  
XX  
XX Use of a cC1qR binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
XX  
XX Claim 9; Page 24-25; 31pp; English.  
PS  
XX This sequence is a C1q and collectin receptor (cC1qR) binding  
CC domain. The invention relates to the use of a cC1qR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB  
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
XX Sequence 122 AA;  
SQ

Query Match 24.6%; Score 69; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.7e-60;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 KPEMDERAKIDDPDTSKPEMDKREHIIPDPAKKPEMDDEMDGEMPEPVIONPEYKGE 137  
DB 54 KPEMDERAKIDDPDTSKPEMDKREHIIPDPAKKPEMDDEMDGEMPEPVIONPEYKGE 113  
OY 138 WKPROIDNP 146  
DB 114 WKPROIDNP 122

RESULT 13  
AAB44058  
ID AAB44058 standard; Protein; 70 AA.  
XX  
AC AAB44058;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated protein sequence SEQ ID NO:1503.  
XX  
KW Human: cancer associated gene; cancer antigen; detection; cancer;  
diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
antidiabetic; antitumor; antineuritic; antitumor; antiviral;  
antitumor; antitumor; antitumor; antitumor; antitumor;  
dermatological; neuroprotective; thrombolytic; coagulant; neotropic;  
vasotropic; antiproliferative; antineoplastic; gene therapy; inflammation;  
immune disorder; haematopoietic cell disorder; autoimmune disorder;  
allergic reaction; graft versus host disease; organ rejection;  
haemostatic; thrombolytic; cardiovascular disorder; infection;  
neurological disease; drug screening.  
OS Homo sapiens.  
PN MO200055350-A1.  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000MO-US05882.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Ruben SM;  
XX WPI: 2000-587533/55.  
DR N-PSDB: AAC78267.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
useful for treating or diagnosing e.g. cancer -  
XX  
PS Claim 11; Page 2179; 2352pp; English.  
XX  
CC AAC77607 to AAC78448 encode the human cancer associated proteins given  
in AAB43398 to AAB44239. The proteins can have activities based on the  
tissues and cells the genes are expressed in. Example of activities  
include: cytostatic; proliferative; vulnery; immunomodulator;  
antidiabetic; antitumor; antineuritic; antitumor; antiviral;  
antitumor; antitumor; antitumor; antitumor; antitumor;  
dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
neotropic; vasotropic; antiproliferative; antineoplastic; gene therapy;  
polynucleotides and polypeptides can be used for preventing, treating or  
ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
the present invention may be used to treat immune disorders by activating  
or inhibiting the proliferation, differentiation or mobilisation of  
immune cells, to treat disorders of haematopoietic cells, autoimmune  
disorders, allergic reactions, graft versus host disease and organ  
rejection, modulate haemostatic or thrombolytic activity, modulate  
inflammation, cancers, cardiovascular disorders, neurological disease and  
bacterial or viral infections. The peptides, nucleotides, antibodies,  
agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
the present invention.  
XX  
SQ Sequence 70 AA;

Query Match 23.9%; Score 67; DB 21; Length 70;  
Best Local Similarity 100.0%; Pred. No. 1e-58;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
AAY92354  
ID AAY92354 standard; Protein; 60 AA.  
XX  
AC AAY92354;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant human calreticulin residues 121-180.  
XX  
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
OS Homo sapiens.  
PN Synthetic.  
PD WO200020577-A1.  
XX  
PF 13-APR-2000.  
XX  
PR 05-OCT-1999; 99WO-US22240.  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PI Tosato G, Pike SE, Yao L;  
XX WPI: 2000-303767/26.  
DR  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
useful for suppressing tumor growth  
XX  
PS Claim 4; Page 85; 99pp; English.  
XX  
CC A novel method of inhibiting endothelial cell growth comprises  
contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
tumor growth and/or endothelial cell growth (claimed). The method may be  
used for inhibiting angiogenesis in a patient. The angiogenesis is  
associated with a disease other than a tumor that is associated with  
neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
trachoma, neovascular glaucoma, psoriasis, angiodermas, immune  
inflammation, atherosclerosis, excessive wound repair, retinal  
neovascularization, macular degeneration, corneal graft rejection,  
contact lens overwear, Crohn's disease, non-immune inflammation,  
rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 60 AA;

Query Match 21.4%; Score 60; DB 21; Length 60;  
Best Local Similarity 100.0%; Pred. No. 8e-52;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPGTKKVVHIFNYKGNKLVINKDIRCKDEFTHLTLIYVPPNTYEKIDNSQVSGSLE 60  
1 GPGTKKVVHIFNYKGNKLVINKDIRCKDEFTHLTLIYVPPNTYEKIDNSQVSGSLE 60

RESULT 15

AA92352  
ID AA92352 standard; Protein: 61 AA.

AC AA92352;

DT 10-AUG-2000 (first entry)

DE Recombinant human calreticulin residues 120-160.

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytosolic; dermalogical; immunosuppressive; anti-inflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.  
OS Synthetic.

PN WO200020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23240.

PR 06-OCT-1998; 98US-0103438.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth

PS Claim 4; Page 82-83; 99pp; English.

CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

SO Sequence 61 AA;

Query Match 21.4%; Score 60; DB 21; Length 61;

Best Local Similarity 100.0%; Pred. No. 8.1e-52;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPGTKKVVHIVNYKGNVLIINKDIRCKDEPETHLYTLIVRPDMYEVKIDNSOVESGSL 60  
2 GPGTKKVVHIVNYKGNVLIINKDIRCKDEPETHLYTLIVRPDMYEVKIDNSOVESGSL 61

Search completed: March 14, 2003, 20:44:21  
Job time : 49.6027 secs



GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 10.3706 Seconds  
(without alignments)  
783.783 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 61  
Sequence: 1 CGPGTKKVVHVFYNGKGNVL.....PDNTYEKIDNSQVSGSLE 61

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	61	100.0	61	21	AA192352	Recombinant human
2	61	100.0	180	21	AA192351	Human vasostatin (
3	61	100.0	400	21	AA192350	Recombinant human
4	61	100.0	401	18	AA111156	Calreticulin, Hom
5	61	100.0	417	10	AA192276	60 kD Ro (Ro/SSA)
6	61	100.0	417	20	AA190927	Calreticulin, Hom
7	61	100.0	417	21	AA192349	Human MBP-calretic
8	61	100.0	417	21	AA192349	Human calreticulin
9	61	100.0	417	23	AA192349	Human calreticulin
10	61	100.0	417	23	AA192349	Human calreticulin

11	60	98.4	60	21	AA192354	Recombinant human
12	60	98.4	280	21	AA192355	Recombinant delta-
13	49	80.3	49	21	AA192353	Recombinant human
14	36	59.0	122	20	AA190924	Human ccl1r binding
15	36	59.0	122	20	AA190926	Rat ccl1r binding
16	19	31.1	122	20	AA190925	Mouse ccl1r binding
17	17	27.9	403	17	AA192349	Human calreticulin
18	13	21.3	406	22	AA192349	Human ovarian anti
19	13	21.3	406	22	AA192349	Drosophila melanog
20	12	19.7	336	12	AA192312	Human calreticulin
21	12	19.7	336	12	AA192312	Partial sequence o
22	9	14.8	9	19	AA192312	Human calreticulin
23	8	13.1	8	19	AA192312	Human calreticulin
24	8	13.1	385	21	AA192353	Human secreted pro
25	7	11.5	400	22	AA192353	Putative P. abyssal
26	7	11.5	591	22	AA192353	Mouse wound healin
27	7	11.5	592	22	AA192353	Human wound healin
28	7	11.5	593	16	AA192353	Calnexin sequence.
29	7	11.5	1009	23	AA192353	Protein of the Bpm
30	7	11.5	1090	22	AA192353	Human protein sequ
31	7	11.5	1394	22	AA192353	Novel human diagno
32	6	9.8	15	20	AA192353	Major epitopic reg
33	6	9.8	15	20	AA192353	Mutant sequence of
34	6	9.8	15	20	AA192353	Mutant sequence of
35	6	9.8	15	20	AA192353	Mutant sequence of
36	6	9.8	15	20	AA192353	Mutant sequence of
37	6	9.8	15	20	AA192353	Mutant sequence of
38	6	9.8	15	20	AA192353	Mutant sequence of
39	6	9.8	33	22	AA192353	Human polypeptide
40	6	9.8	46	22	AA192353	Novel human diagno
41	6	9.8	62	20	AA192353	Secreted protein e
42	6	9.8	64	22	AA192353	Human polypeptide
43	6	9.8	69	23	AA192353	Staphylococcus epi
44	6	9.8	70	20	AA192353	Human normal blad
45	6	9.8	74	23	AA192353	Staphylococcus epi

## ALIGNMENTS

RESULT 1	
AA192352	
ID	AA192352 standard; Protein: 61 AA.
AC	AA192352;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Recombinant human calreticulin residues 120-180.
XX	
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW	cytoskeletal; dermatological; immunosuppressive; anti-inflammatory; hepatic;
KW	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX	
OS	Homo sapiens.
XX	
PN	Synthetic.
XX	
WO	WO200020577-A1.
XX	
PD	13-APR-2000.
XX	
PF	05-OCT-1999; 99WO-US23240.
XX	
PR	06-OCT-1998; 98US-0103438.
XX	
PA	(USSS ) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Tosato G, Pike SE, Yao L;
XX	
DR	WPI; 2000-303767/26.
XX	
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth  
XX  
XX Claim 4; Page 82-83; 99pp; English.  
PS  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
CC  
SQ Sequence 61 AA:  
DB  
QY 1 CGPGTKKVVHIFNYKGNVLIINKDIRCKDEFTHTLTLVPRDNTYEKIDNSQVESGSL 60  
1 CGPGTKKVVHIFNYKGNVLIINKDIRCKDEFTHTLTLVPRDNTYEKIDNSQVESGSL 60  
DB 1 CGPGTKKVVHIFNYKGNVLIINKDIRCKDEFTHTLTLVPRDNTYEKIDNSQVESGSL 60  
QY 61 E 61  
DB 61 E 61  
DB 61 E 61  
RESULT 2  
AAV92351  
ID AAV92351 standard; Protein; 180 AA.  
AC AAV92351;  
XX  
XX 10-AUG-2000 (first entry)  
DT  
XX Human vasostatin (calreticulin N-terminal 180 amino acids).  
DE  
XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;  
XX angiogenesis; inhibition; endothelial cell; anti-angiogenic;  
XX neuroprotective; antidiabetic; cyostatic; dermatological; hepatic;  
XX immunosuppressive; anti-inflammatory; anti-atherosclerotic;  
XX gastrointestinal; anti-arthritis; ophthalmic.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200020577-A1.  
PN  
XX 13-APR-2000.  
PD  
XX 05-OCT-1999; 99WO-US23240.  
PF  
XX 06-OCT-1998; 98US-0103438.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Tosato G, Pike SE, Yao L;  
PI  
XX WPI; 2000-303767/26.  
DR  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
PS Claim 4; Page 82; 99pp; English.

XX  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
CC  
SQ Sequence 180 AA:  
DB  
QY 1 CGPGTKKVVHIFNYKGNVLIINKDIRCKDEFTHTLTLVPRDNTYEKIDNSQVESGSL 60  
120 CGPGTKKVVHIFNYKGNVLIINKDIRCKDEFTHTLTLVPRDNTYEKIDNSQVESGSL 179  
DB 120 CGPGTKKVVHIFNYKGNVLIINKDIRCKDEFTHTLTLVPRDNTYEKIDNSQVESGSL 179  
QY 61 E 61  
DB 61 E 61  
DB 180 E 180  
RESULT 3  
AAV92350  
ID AAV92350 standard; Protein; 400 AA.  
AC AAV92350;  
XX  
XX 10-AUG-2000 (first entry)  
DT  
XX Recombinant human MBP-calreticulin.  
DE  
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
XX endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
XX cyostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;  
XX anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
XX Homo sapiens.  
OS  
XX WO200020577-A1.  
PN  
XX 13-APR-2000.  
PD  
XX 05-OCT-1999; 99WO-US23240.  
PF  
XX 06-OCT-1998; 98US-0103438.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Tosato G, Pike SE, Yao L;  
PI  
XX WPI; 2000-303767/26.  
DR  
XX N-PSDB; AAA09346, AAA09347.  
DR  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
PS Claim 4; Page 80-81; 99pp; English.  
PS  
CC Recombinant human MBP-calreticulin comprises the sequence of human  
CC calreticulin (see AAV92349) without the 17 N-terminal amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises



CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).

XX Sequence 400 AA;

Query Match 100.0%; Score 61; DB 21; Length 400;

Best Local Similarity 100.0%; Pred. No. 3.2e-62;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKVHVIFNFKGNVLINKDIRCKDDETHLYTLIVRPDNTYEKIDNSQVSGSL 60

Db 120 CGPGTKVHVIFNFKGNVLINKDIRCKDDETHLYTLIVRPDNTYEKIDNSQVSGSL 179

OY 61 E 61

Db 180 E 180

RESULT 4

AAW11156 standard; peptide: 401 AA.

AC AAW11156;

DT 31-MAY-1997 (first entry)

DE Calreticulin.

KW calreticulin; C-domain; restenosis; inhibitor.

OS Homo sapiens.

PN W09636643-A1.

PD 21-NOV-1996.

PE 17-MAY-1996; 96WO-IB00471.

PR 16-MAY-1996; 96US-0649417.

PR 17-MAY-1995; 95US-0442844.

PA (UYAL-) UNIV ALBERTA.

PI Lucas A, Michalak M;

DR WPI; 1997-012036/01.

PT Inhibition of restenosis in patients - using calreticulin or a

PT C-domain polypeptide of calreticulin or a variant with the same

PT activity.

PS Disclosure; Fig 1; 48pp; English.

CC The present sequence is calreticulin. It and a C-domain derived peptide  
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The  
 CC calreticulin-type cpds. are administered either parenterally,  
 CC intravenously or via a catheter and can target areas of vascular damage  
 CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

Query Match 100.0%; Score 61; DB 18; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-62;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKVHVIFNFKGNVLINKDIRCKDDETHLYTLIVRPDNTYEKIDNSQVSGSL 60

Db 120 CGPGTKVHVIFNFKGNVLINKDIRCKDDETHLYTLIVRPDNTYEKIDNSQVSGSL 179

OY 61 E 61

Db 180 E 180

RESULT 5

AAP92276 standard; protein: 417 AA.

AC AAP92276;

DT 23-FEB-1990 (first entry)

DE 60 kD Ro (Ro/SSA) antigen.

KW Sjorens syndrome; systemic lupus erythematosus.

OS Synthetic.

PN W08909273-A.

PD 05-OCT-1989.

PE 22-MAR-1989; 89WO-US01213.

PR 22-MAR-1988; 88US-0171634.

PA (TEXA) UNIV OF TEXAS SYST.

PI Sontheimer RD, Capra JD, McCauliffe DP;

DR WPI; 1989-309537/42.

DR N-PSDB; AAP92276.

PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen

PT - used in immunoassays to detect rheumatic disease

PS Disclosure; Fig 2; 88pp; English.

CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
 CC expressed recombinantly to detect autoantibodies, for identification  
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,  
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
 CC antigens.

XX Sequence 417 AA;

Query Match 100.0%; Score 61; DB 10; Length 417;

Best Local Similarity 100.0%; Pred. No. 3.3e-62;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKVHVIFNFKGNVLINKDIRCKDDETHLYTLIVRPDNTYEKIDNSQVSGSL 60

Db 137 CGPGTKVHVIFNFKGNVLINKDIRCKDDETHLYTLIVRPDNTYEKIDNSQVSGSL 196

OY 61 E 61

Db 197 E 197

RESULT 6

AAV00927 standard; Protein: 417 AA.

XX ID AAV00927

AC AAY00927;  
XX  
XX 28-MAY-1999 (first entry)  
XX  
DE Calreticulin.  
XX  
XX C1q and collectin receptor; cclqr binding domain; complement ubiquitin;  
KM CUB functional; inhibitor; complement activation; inflammation;  
KM myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KM rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
XX immune complex nephritis; therapy.  
XX  
OS Homo sapiens.  
XX  
XX WO9907406-A1.  
XX  
XX 18-FEB-1999.  
XX  
XX 12-AUG-1998; 98WO-GB02430.  
XX  
XX 12-AUG-1997; 97GB-0016998.  
XX  
XX (UYLE-) UNITV LEICESTER.  
XX  
XX Schwaedle W;  
XX  
XX WPI; 1999-180404/15.  
XX  
XX Use of a cclqr binding domain - to modulate complement ubiquitin  
XX (CUB) functionality.  
XX  
XX Disclosure: Page 26-27; 31pp; English.  
XX  
XX This sequence is calreticulin, a homologue of C1q and collectin receptor  
XX (CCQR). The invention relates to the use of a cclqr binding domain in a  
XX medicament to effect complement ubiquitin (CUB) functionality, and an  
XX inhibitor of the cclqr binding domain in a medicament to inhibit CUB  
XX functionality. The cclqr binding domain, or its inhibitor, can be used to  
XX treat a human or animal body. Particularly an inhibitor is used to treat  
XX inflammation, for example in myocardial infarction, brain ischaemia  
XX (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
XX erythematosus, burns, immune complex nephritis, and to treat amyloid  
XX plaques in Alzheimer's disease. The use of cclqr binding domain or  
XX inhibitor enables the CUB domain functionality to be modulated using a  
XX low molecular weight molecule.  
XX  
SQ Sequence 417 AA:  
Query Match 100.0%; Score 61; DB 20; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.3e-62;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGPGTKKVVHVFNYKGNVINKDKRCKDEFTHTLTLVLRPDNTYEKINDSYESGSL 60  
DB 137 CGPGTKKVVHVFNYKGNVINKDKRCKDEFTHTLTLVLRPDNTYEKINDSYESGSL 196  
QY 61 E 61  
DB 197 E 197

RESULT 7  
ID AAY92349 standard; Protein; 417 AA.  
XX  
XX AAY92349;  
XX  
XX 10-AUG-2000 (first entry)  
XX  
XX Human MBP-calreticulin.  
XX  
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KM cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..17  
XX Protein 18  
XX /label= mature\_protein  
XX  
XX WO200020577-A1.  
XX  
XX 13-APR-2000.  
XX  
XX 05-OCT-1999; 99WO-US23240.  
XX  
XX 06-OCT-1998; 98US-0103438.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Tosato G, Pike SE, Yao L;  
XX  
XX WPI; 2000-303767/26.  
XX  
XX N-PSDB; AAA09346, AAA09347.  
XX  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
XX useful for suppressing tumor growth  
XX  
XX Disclosure: Page 79-80; 99pp; English.  
XX  
XX A novel method of inhibiting endothelial cell growth comprises  
XX contacting the cells with calreticulin (or its fragments/variants).  
XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
XX tumor growth and/or endothelial cell growth (claimed). The method may be  
XX used for inhibiting angiogenesis in a patient. The angiogenesis is  
XX associated with a disease other than a tumor that is associated with  
XX neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
XX trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
XX inflammation, atherosclerosis, excessive wound repair, retinal  
XX neovascularization, macular degeneration, corneal graft rejection,  
XX contact lens overwear, Crohn's disease, non-immune inflammation,  
XX rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
XX Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
XX syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
XX also be used for treating/inhibiting tumor growth especially  
XX kaposi's sarcoma (claimed).  
XX  
SQ Sequence 417 AA:  
Query Match 100.0%; Score 61; DB 21; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.3e-62;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGPGTKKVVHVFNYKGNVINKDKRCKDEFTHTLTLVLRPDNTYEKINDSYESGSL 60  
DB 137 CGPGTKKVVHVFNYKGNVINKDKRCKDEFTHTLTLVLRPDNTYEKINDSYESGSL 196  
QY 61 E 61  
DB 197 E 197

RESULT 8  
ID AAE24591 standard; Protein; 417 AA.  
XX  
XX AAE24591;  
XX  
XX 04-OCT-2002 (first entry)  
XX  
XX Human calreticulin protein.

XX Human; calreticulin; antisense compound; hyperproliferative disorder;  
KW cancer; autoimmune disease; viral infection; cardiovascular disease;  
KM antisense therapy; cytostatic; immunosuppressive; virocidine.  
OS Homo sapiens.  
PN WO200236743-A2.  
XX  
XX  
PD 10-MAY-2002.  
XX  
XX 30-OCT-2001; 2001WO-US49045.  
XX  
XX 30-OCT-2000; 2000US-0702327.  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA Bennett CF, Cowser LM;  
PI  
XX  
XX WPI; 2002-479759/51.  
DR N-PSDB: AAD39469.  
XX  
XX Novel antisense compound targeted to nucleic acid encoding  
PT calreticulin, useful for treating a human having disease or condition  
PT associated with calreticulin e.g. cancer, viral infection, autoimmune  
PT disease -  
XX  
XX  
PS Disclosure: Page 88-90; 109pp; English.  
XX  
XX The invention relates to antisense compounds, compositions and methods  
CC for modulating the expression of calreticulin. The compositions comprise  
CC antisense compounds, particularly antisense oligonucleotides, targeted  
CC to nucleic acids encoding calreticulin. The antisense compound is useful  
CC for inhibiting the expression of calreticulin in human cells or tissues.  
CC It is also useful for treating a human having a disease or condition  
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.  
CC cancer, autoimmune disease, viral infection or cardiovascular disease,  
CC by inhibiting expression of calreticulin. It is useful for diagnostics,  
CC therapeutics, prophylaxis and as research reagents and kits. It is also  
CC used in antisense therapy. The present sequence is human calreticulin  
CC protein. This sequence is used in the exemplification of the invention.  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 61; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.3e-62;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGPGTKKVVIVNYKKNVLYNKDKRDEFTHTLTVLRPNTEYEVKIDNSQVESGSL 60  
DB 137 CGPGTKKVVIVNYKKNVLYNKDKRDEFTHTLTVLRPNTEYEVKIDNSQVESGSL 196  
QY 61 E 61  
DB 197 E 197  
RESULT 9  
AAU77712  
ID AAU77712 standard; Protein; 417 AA.  
XX  
XX AAU77712;  
AC  
XX  
DT 05-JUN-2002 (first entry)  
XX  
XX Human calreticulin (CRT).  
XX  
XX Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;  
KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;  
KM enhanced antigen-specific immune response; cytotoxic T lymphocyte;  
KW tumour; cancer; cervical cancer.  
XX  
XX Homo sapiens.

XX  
PN WO200212281-A2.  
XX  
XX 14-FEB-2002.  
XX  
XX 02-AUG-2001; 2001WO-US24134.  
XX  
XX 03-AUG-2000; 2000US-222902P.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA Wu T, Hung C;  
PI  
XX  
XX WPI; 2002-257463/30.  
DR N-PSDB: ABE11662.  
XX  
XX New nucleic acids encoding a fusion polypeptide comprising an  
PT endoplasmic reticulum chaperone polypeptide linked to an antigenic  
PT polypeptide, useful as a vaccine for inducing antigen-specific immune  
PT responses -  
XX  
XX  
PS Disclosure: Page 27; 71pp; English.  
XX  
XX The invention describes a nucleic acid molecule (I) encoding a fusion  
CC polypeptide comprising a first polypeptide domain comprising an  
CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and  
CC a second polypeptide domain comprising at least one antigenic peptide  
CC e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as  
CC a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune  
CC responses, particularly those mediated by cytotoxic T lymphocytes. The  
CC nucleic acid and compositions comprising the nucleic acid is also useful  
CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.  
CC This is the amino acid sequence of the human calreticulin (CRT), an  
CC endoplasmic reticulum protein used in the creation of a DNA vaccine.  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 61; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.3e-62;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGPGTKKVVIVNYKKNVLYNKDKRDEFTHTLTVLRPNTEYEVKIDNSQVESGSL 60  
DB 137 CGPGTKKVVIVNYKKNVLYNKDKRDEFTHTLTVLRPNTEYEVKIDNSQVESGSL 196  
QY 61 E 61  
DB 197 E 197  
RESULT 10  
AAE18851  
ID AAE18851 standard; Protein; 417 AA.  
XX  
XX AAE18851;  
AC  
XX  
DT 17-MAY-2002 (first entry)  
XX  
XX Human calreticulin protein.  
XX  
XX Human; prostate cancer; calreticulin; T1D-1 protein; TRAITS protein;  
KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;  
KM epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;  
KW cytosolic; v19 protein.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 98..170  
FT Domain /Label= N-terminal\_domain  
FT 98..103  
FT Region /Label= Alpha\_helix  
FT 149..154  
FT Region

```
FT Domain /label= Alpha_helix
FT 171..285 /note= "Proline-rich domain (P domain)"
FT Domain 286..397
FT /label= C-terminal_domain
XX WO200206327-A2.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-US22357.
XX
XX 17-JUL-2000; 2000US-218761P.
XX 16-JUL-2001; 2001US-0906393.
XX
XX (NOON ) UNIV NORTHWESTERN.
XX
XX Wang Z, Xiao W;
XX
XX WPI: 2002-179780/23.
XX N-PSDB; AAD29931.
XX
XX Identifying a subject that is likely to have aggressive form of
XX prostate cancer, involves comparing calreticulin levels in prostate
XX specimen of the subject and in benign prostatic epithelial cells of the
XX same subject
XX
XX Disclosure: Page 146-148; 148pp; English.
XX
XX The present invention relates to methods of distinguishing aggressive
XX forms of prostate cancer from non-aggressive forms. The method involves
XX comparing the level of calreticulin in prostate specimen and in benign
XX prostatic epithelial cells of a subject. The invention particularly
XX relates to two proteins, namely calreticulin and RID-1 (PRAIRIS: 019)
XX that are down-regulated in aggressive forms of prostate cancer but not
XX in slowly progressing prostate cancer. They play important roles in
XX the part of androgen action pathway that suppresses cell proliferation
XX and/or prevents prostate cancer. The method is useful for identifying
XX a subject who is likely to have an aggressive form of prostate cancer.
XX The invention further relates to a method of identifying a subject with
XX a slow growing form of prostate cancer. T1D-1 sequences are useful for
XX treating cancers such as epithelium-derived carcinomas, kidney cancers,
XX lymphomas, leukaemias and prostate cancers. Sequences of the invention
XX are used as vaccines and in gene therapy. The present sequence is human
XX calreticulin protein.
XX
XX Sequence 417 AA:
XX
XX Query Match 100.0%; Score 61; DB 23; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-62;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGPGTKKVVHVFNYKGNVLINRKDKDEFTHLVTLIVRPNTYEVKIDNSQVESGSL 60
XX |||||||
XX DB 137 CGPGTKKVVHVFNYKGNVLINRKDKDEFTHLVTLIVRPNTYEVKIDNSQVESGSL 196
XX
XX QY 61 E 61
XX
XX DB 197 E 197
XX
XX RESULT 11
XX AAY92354
XX ID AAY92354 standard; Protein; 60 AA.
XX
XX AC AAY92354;
XX
XX 10-AUG-2000 (first entry)
XX
XX Recombinant human calreticulin residues 121-180.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX
```

```
KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US23240.
XX
XX 06-OCT-1998; 98US-0103438.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
XX
XX WPI: 2000-303767/26.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX useful for suppressing tumor growth
XX
XX Claim 4; Page 85; 99pp; English.
XX
XX A novel method of inhibiting endothelial cell growth comprises
XX contacting the cells with calreticulin (or its fragments/variants).
XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
XX tumor growth and/or endothelial cell growth (claimed). The method may be
XX used for inhibiting angiogenesis in a patient. The angiogenesis is
XX associated with a disease other than a tumor that is associated with
XX neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
XX trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune
XX inflammation, atherosclerosis, excessive wound repair, retinal
XX neovascularization, macular degeneration, corneal graft rejection,
XX contact lens overwear, Crohn's disease, non-immune inflammation,
XX rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
XX Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX also be used for treating/inhibiting tumor growth especially
XX Kaposi's sarcoma (claimed).
XX
XX Sequence 60 AA:
XX
XX Query Match 98.4%; Score 60; DB 21; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-62;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GPGTKKVVHVFNYKGNVLINRKDKDEFTHLVTLIVRPNTYEVKIDNSQVESGSL 61
XX |||||||
XX DB 1 GPGTKKVVHVFNYKGNVLINRKDKDEFTHLVTLIVRPNTYEVKIDNSQVESGSL 60
XX
XX RESULT 12
XX AAY92355
XX ID AAY92355 standard; Protein; 280 AA.
XX
XX AC AAY92355;
XX
XX 10-AUG-2000 (first entry)
XX
XX Recombinant delta-120 calreticulin.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO200020577-A1.
XX
```

PD 13-APR-2000.  
XX  
XX 05-OCT-1999; 99WO-US23240.  
PF  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
XX  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Tosato G, Pike SE, Yao L;  
PI  
XX WPI; 2000-303767/26.  
DR  
XX  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
XX  
PS Claim 4; Page 86; 99pp; English.  
XX  
XX This sequence comprises recombinant human calreticulin (AA92350)  
CC missing the N-terminal 120 amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The  
CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 280 AA:  
  
Query Match 98.4%; Score 60; DB 21; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-61;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 2 GPGTKRVHYIFNFKGNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVSGSLE 61  
DB 1 GPGTKRVHYIFNFKGNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVSGSLE 60  
  
RESULT 13  
AA92353  
ID AAY92353 standard; Protein: 49 AA.  
XX  
XX AAY92353;  
AC  
XX  
XX 10-AUG-2000 (first entry)  
DE  
XX  
XX Recombinant human calreticulin residues 132-180.  
XX  
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytotoxic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Synthetic.  
PN  
XX WO200020577-A1.  
XX  
XX 13-APR-2000.  
PD  
XX  
XX 05-OCT-1999; 99WO-US23240.  
PF  
XX  
XX 06-OCT-1998; 98US-0103438.  
PR  
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Tosato G, Pike SE, Yao L;  
PI  
XX WPI; 2000-303767/26.  
DR  
XX  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
XX  
PS Claim 4; Page 82-83; 99pp; English.  
XX  
XX A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 49 AA:  
  
Query Match 80.3%; Score 49; DB 21; Length 49;  
Best Local Similarity 100.0%; Pred. No. 3.6e-49;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 13 NYKGNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVSGSLE 61  
DB 1 NYKGNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVSGSLE 49  
  
RESULT 14  
AAY00924  
ID AAY00924 standard; Protein: 122 AA.  
XX  
XX AAY00924;  
AC  
XX  
XX 28-MAY-1999 (first entry)  
DE  
XX  
XX Human cC1qR binding domain protein sequence.  
XX  
XX C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischemia; gut ischemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9907406-A1.  
PN  
XX  
XX 18-FEB-1999.  
PD  
XX  
XX 12-AUG-1998; 98WO-GB02430.  
PF  
XX  
XX 12-AUG-1997; 97GB-0016998.  
PR  
XX  
XX (UYLE-) UNIV LEICESTER.  
PA  
XX  
XX Schwaebler W;  
PI  
XX  
XX WPI; 1999-180404/15.  
DR  
XX  
XX N-PSDB; AAX27251.  
DR  
XX  
XX Use of a cC1qR binding domain - to modulate complement ubiquitin  
PT

PT (CUB) functionality.  
XX  
PS Claim 9; Page 23; 31pp; English.  
XX  
CC This sequence is a C1q and collectin receptor (CC1qR) binding  
CC domain. The invention relates to the use of a cC1qR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB  
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
SQ Sequence 122 AA:  
  
Query Match 59.0%; Score 36; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1e-33;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 26 RCKDDEFTHLVTLVPRDNTYEKIDNSQVSGSLE 61  
DB 1 RCKDDEFTHLVTLVPRDNTYEKIDNSQVSGSLE 36  
  
RESULT 15  
AA00926  
ID AA00926 standard; Protein; 122 AA.  
XX  
AC AA00926;  
XX  
DT 28-MAY-1999 (first entry)  
XX  
DE Rat cC1qR binding domain protein sequence.  
XX  
KW C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
OS Rattus norvegicus.  
XX  
PN WO9907406-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 12-AUG-1998; 98WO-GB02430.  
XX  
PR 12-AUG-1997; 97GB-0016998.  
XX  
PA (UYLE-) UNTV LEICESTER.  
XX  
PI Schwaebler W;  
XX  
DR WPI: 1999-180404/15.  
DR N-PSDB; AAX27253.  
XX  
XX  
PT Use of a cC1qR binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
XX  
PS Claim 9; Page 24-25; 31pp; English.  
XX  
CC This sequence is a C1q and collectin receptor (cC1qR) binding  
CC domain. The invention relates to the use of a cC1qR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB  
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat

CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
SQ Sequence 122 AA:  
  
Query Match 59.0%; Score 36; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1e-33;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 26 RCKDDEFTHLVTLVPRDNTYEKIDNSQVSGSLE 61  
DB 1 RCKDDEFTHLVTLVPRDNTYEKIDNSQVSGSLE 36

Search completed: March 14, 2003, 20:44:18  
Job time : 11.3706 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 4.36963 Seconds  
(without alignments)  
1342.037 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 61

Sequence: 1 CGPGTKKVVHVFNFYKGNVL.....PDNTYEYKIDNSQVESGSL 61

Scoring table: OLIGO

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	416	1 S06763	calreticulin precu
2	61	100.0	416	2 JH0819	calreticulin precu
3	61	100.0	417	1 A37047	calreticulin precu
4	61	100.0	418	1 A34154	calreticulin precu
5	42	68.9	400	2 S43376	calreticulin, bra
6	42	68.9	421	2 S36799	calreticulin precu
7	22	36.1	384	2 S29130	calreticulin (clon
8	22	36.1	411	2 S29129	calreticulin precu
9	20	32.8	419	2 S71343	calreticulin precu
10	19	31.1	405	1 JH0795	calreticulin precu
11	14	23.0	393	1 A48573	calreticulin autoa
12	13	21.3	406	2 A56637	calreticulin homol
13	12	19.7	336	2 A32507	41k larval antigen
14	9	14.8	395	2 S25851	calreticulin precu
15	7	11.5	93	2 A25343	nonhistone chromos
16	7	11.5	93	2 S05243	nonhistone chromos
17	7	11.5	93	2 S13717	histone-like prote
18	7	11.5	358	2 T12850	hypothetical prote
19	7	11.5	397	2 C75182	DNA-directed RNA p
20	7	11.5	397	2 G71031	probable DNA-direc
21	7	11.5	414	2 T39450	phosphoglycerate k
22	7	11.5	591	2 B54354	calnexin precursor
23	7	11.5	591	2 C54354	calnexin precursor
24	7	11.5	592	2 T53260	calnexin - human
25	7	11.5	592	2 A46673	calnexin precursor
26	7	11.5	593	2 A37273	calnexin precursor
27	7	11.5	1461	2 E84589	probable retroelem
28	6	9.8	19	2 S54848	succinyl-CoA synth
29	6	9.8	81	2 P97347	transition state r

30	6	9.8	87 2 B34455
31	6	9.8	89 2 A34455
32	6	9.8	90 2 C34455
33	6	9.8	97 2 H69440
34	6	9.8	103 2 F75010
35	6	9.8	109 2 E64473
36	6	9.8	144 2 A96580
37	6	9.8	146 2 S66060
38	6	9.8	152 2 T18975
39	6	9.8	160 2 C84279
40	6	9.8	173 2 AC3503
41	6	9.8	187 2 T25461
42	6	9.8	196 2 S63429
43	6	9.8	203 2 H96525
44	6	9.8	214 2 T49758
45	6	9.8	218 1 RTHUG

## ALIGNMENTS

RESULT 1  
S06763

calreticulin precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999

C:Accession: S06763; JCI444; PGI233; A57498

R:Smith, M.J.; Koch, G.L.E.

EMBO J. 8, 3581-3586, 1989

A:Title: Multiple zones in the sequence of calreticulin (CRP5, calregulin, HACBP), a

A:Reference number: S06763; MUID:90059555; PMID:2583110

A:Accession: S06763

A:Molecule type: DNA

A:Residues: 1-416 <SMT>

A:Cross-references: EMBL:X14926; NID:g50567; PIDD:CAA33053.1; PID:g50568

R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.

Gene 120, 217-225, 1992

A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca

A:Reference number: JCI444; MUID:93013037; PMID:1398135

A:Accession: JCI444

A:Molecule type: mRNA

A:Residues: 1-416 <MAZ>

A:Cross-references: GB:M92988; NID:g193084; PIDD:AAA37569.1; PID:g193085

A:Accession: PGI233

A:Molecule type: Protein

A:Residues: 18-41 <MAZ>

R:White, T.K.; Zhu, O.; Tanzer, M.L.

J. Biol. Chem. 270, 15926-15929, 1995

A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mous

A:Reference number: A57498; MUID:9532280; PMID:7608143

A:Accession: A57498

A>Status: preliminary

A:Molecule type: protein

A:Residues: 74-80;142-151;186-193 <WHT>

C:Superfamily: calreticulin

C:Keywords: calcium binding

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-416/Product: calregulin #status experimental <MAT>

F:413-416/Region: endoplasmic reticulum retention signal

Query Match

Best Local Similarity 100.0%; Score 61; DB 1; Length 416;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGPGTKKVVHVFNFYKGNVLKIDRCKDEPTHTLTLIVRPDNYEVKIDNSQVESGSL 60
DB	137	CGPGTKKVVHVFNFYKGNVLKIDRCKDEPTHTLTLIVRPDNYEVKIDNSQVESGSL 196
QY	61	E 61
DB	197	E 197

## RESULT 2

JH0819  
 Calreticulin precursor - rat  
 N:Alternate names: calcium-binding protein 3  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence-revision 20-Aug-1994 #text-change 20-Jun-2000  
 C:Accession: JH0819; A49176; S11205; P01109; S45036; S04867; S39372; A34473; S13045  
 R:Nakamura, M.; Moriya, M.; Baba, T.; Mchikawa, Y.; Yamanohe, T.; Arai, K.; Okinaga, S.  
 Exp. Cell Res. 205, 101-110, 1993  
 A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom  
 A:Reference number: A49176; MUID:93202172; PMID:9453984  
 A:Accession: JH0819  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <NAK>  
 A:Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:91845572  
 A:Accession: A49176  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <NAK>  
 A:Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:91845572  
 A:Accession: A49176  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-416 <NAK>  
 A:Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:91845572  
 A:Experimental source: Sprague-Dawley, spermatogenic cells  
 A:Note: sequence extracted from NCBI backbone (NCBIN:127633, NCBIP:127643)  
 R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y  
 Nucleic Acids Res. 18, 4933, 1990  
 A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc  
 A:Reference number: S11205; MUID:90370496; PMID:2395661  
 A:Accession: S11205  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <NAK>  
 A:Cross-references: EMBL:X53363; NID:955854; PIDN:CAA37446.1; PID:955855  
 R:Nakamura, M.; Mchikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
 A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.  
 A:Reference number: P01109; MUID:92360010; PMID:1497655  
 A:Accession: P01109  
 A:Molecule type: protein  
 A:Residues: 18-32 <NAK2>  
 A:Experimental source: testis, strain Sprague-Dawley  
 R:Soenichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes  
 submitted to the EMBL Data Library, May 1994  
 A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul  
 A:Reference number: S45036  
 A:Accession: S45036  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <SOB>  
 A:Cross-references: EMBL:X79327; NID:9488840; PIDN:CAA55890.1; PID:9488841  
 R:Lone, Y.C.; Bailly, A.; Laruffe, N.  
 submitted to the EMBL Data Library, December 1988  
 A:Reference number: S04867  
 A:Accession: S04867  
 A:Molecule type: mRNA  
 A:Residues: 'R', 270-358, 'AAG' <LON>  
 A:Cross-references: EMBL:X13702; NID:956055; PIDN:CAA31987.1; PID:956055  
 A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
 R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horinuchi, R.; Kametaki, T.  
 Biochim. Biophys. Acta 1158, 333-344, 1993  
 A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an  
 A:Reference number: S39371; MUID:94072621; PMID:8251535  
 A:Accession: S39372  
 A:Molecule type: protein  
 A:Residues: 18-23, 'X', 25-32 <YOK>  
 R:Van, P.N.; Peter, F.; Soeling, H.D.  
 J. Biol. Chem. 264, 17494-17501, 1989  
 A:Title: Four intracellular calcium-binding glycoproteins from rat liver microsomes wit  
 itive calcium sequestering rat liver vesicles  
 A:Reference number: A34473; MUID:90008920; PMID:2793869  
 A:Accession: A34473  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-36 <VAN>  
 R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld

Biochem. J. 271, 473-480, 1990  
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
 A:Reference number: S13045; MUID:91054414; PMID:2241926  
 A:Accession: S13045  
 A:Molecule type: protein  
 A:Residues: 18-29 <TRB>  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding; glycoprotein  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-416/Product: calreticulin #status experimental <MAN>  
 F:204-212/Region: nuclear location signal  
 F:413-416/Region: endoplasmic reticulum retention signal  
 F:344/Binding site: carbohydrate (asn) (covalent) #status predicted  
 Query Match 100.0%; Score 61; DB 2; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 8,4e-57;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPGRKRVIVINNYGKNVINKDKRCKDDETHLYTLVLRDNTYEVKINDSOYEGSGL 60  
 Db 137 CGPGRKRVIVINNYGKNVINKDKRCKDDETHLYTLVLRDNTYEVKINDSOYEGSGL 196  
 QY 61 E 61  
 Db 197 E 197  
 RESULT 3  
 A37047  
 Calreticulin precursor - human  
 N:Alternate names: 52k ribonucleoprotein autoantigen Ro/SS-A; 60k integrin-binding pr  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 18-Feb-2000  
 C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
 R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.  
 J. Biol. Chem. 267, 2557-2562, 1992  
 A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
 A:Reference number: A42330; MUID:92129342; PMID:1733953  
 A:Accession: A42330  
 A:Molecule type: DNA  
 A:Residues: 1-417 <MC2>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)  
 R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
 J. Clin. Invest. 85, 1379-1391, 1990  
 A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
 A:Reference number: A37047; MUID:90237213; PMID:2332496  
 A:Accession: A37047  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <MC2>  
 A:Cross-references: GB:M32294; NID:9337486; PIDN:AAA36582.1; PID:9337487  
 A:Note: the authors translated the codon GTA for residue 349 as Tyr  
 R:Rokach, L.A.; Haselby, J.A.; Mellor, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.  
 J. Immunol. 147, 3031-3039, 1991  
 A:Title: Characterization of the autoantigen calreticulin.  
 A:Reference number: A46452; MUID:92013129; PMID:1919005  
 A:Accession: A46452  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <ROK>  
 A:Cross-references: GB:M44739; NID:9179881; PIDN:AAA51916.1; PID:9179882  
 A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)  
 R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.  
 J. Clin. Invest. 82, 96-101, 1988  
 A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence  
 A:Reference number: A28812; MUID:88273610; PMID:3260607  
 A:Accession: A28812  
 A:Molecule type: protein  
 A:Residues: 18-41 <LIE>  
 A:Note: 18-Ala was also found  
 R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschoep, J.  
 J. Exp. Med. 177, 1-7, 1993  
 A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
 A:Reference number: PH1525; MUID:93115648; PMID:8418194  
 A:Accession: PH1525



```

A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A>Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calreticulin)
A:Reference number: A40346; MUID:92002034; PMID:1911778
A:Accession: A40346
A:Molecule type: protein
A:Residues: 18-34,'R' <ROJ>
R:Krause, K.H.; Slammerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem J. 270, 545-548, 1990
A>Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purified with
A:Reference number: S11475; MUID:90380058; PMID:2400400
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R:Ramerdin, J.; McCready, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.
submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region
A:Reference number: 222906
A:Accession: T45075
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AA851176.1
A:Experimental source: cell line SHL2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and
C:Genetics:
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CRIC
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 61; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 8.5e-57;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKRVHVFNYNGKVVNLINKDIRCKDDEFTHLTYLIVRPDNTYEKINSOVESGSL 60
DB 137 CGPGTKKRVHVFNYNGKVVNLINKDIRCKDDEFTHLTYLIVRPDNTYEKINSOVESGSL 196

OY 61 E 61
DB 197 E 197

RESULT 4
A34154
calreticulin precursor, skeletal muscle - rabbit
A:Residues: 1-418 <FLU>
A:Cross-references: GB:J05138; NID:q164858; PIDN:AAA31188.1; PID:q164859
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34154; S13047
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A>Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c
A:Reference number: A34154; MUID:90094320; PMID:2600080
A:Accession: A34154
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLU>
A:Cross-references: GB:J05138; NID:q164858; PIDN:AAA31188.1; PID:q164859
R:Traves, S.; de Mattei, M.; Lanfredi, M.; Valla, A.; Green, N.M.; MacLennan, D.H.; Meldal
Biochem J. 271, 473-480, 1990
A>Title: Calreticulin is a candidate for a calcequestrin-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13047

```

```

A:Molecule type: protein
A:Residues: 19-32 <TRP>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <SIG>
F:415-418/Region: endoplasmic reticulum retention signal

Query Match          100.0%; Score 61; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 8,5e-57;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CGPGTKKVVHVFNNYKGKNVLLINKDIRCKDDEFTHLTYLIVRPDMTEYVKIDINSQVESGL 60
        |||||||
Db       137 CGPGTKKVVHVFNNYKGKNVLLINKDIRCKDDEFTHLTYLIVRPMNTYEYKIDINSQVESGL 196

Oy      61 E 61
        |
Db       197 E 197

RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C:Accession: S43376; S36801
R:Matsumoto, K.; Seto, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isohe, T.
Biochem. J. 299, 435-442, 1994
A>Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A>Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match          68.9%; Score 42; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1,1e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CGPGTKKVVHVFNNYKGKNVLLINKDIRCKDDEFTHLTYLIVRP 42
        |||||||
Db       120 CGPGTKKVVHVFNNYKGKNVLLINKDIRCKDDEFTHLTYLIVRP 161

RESULT 6
S36799
calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C:Accession: S36799; S36800
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A>Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LIU>
A:Cross-references: GB:LI3462; NID:g348693; PIDN:AAC37307.1; PID:g348694
A:Experimental source: brain, clone 9.4
```

A:Accession: S36800  
A:Molecule type: protein  
A:Residues: 35-45 <LI2>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>  
F:418-421/Region: endoplasmic reticulum retention signal  
F:141-167/Disulfide bonds: #status predicted  
F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.9%; Score 42; DB 2; Length 421;  
Best Local Similarity 100.0%; Pred. No. 1.1e-36;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHVFYKGNVLIKDKRCKDEFFHLYTLIVRP 42  
DB 141 CGPGTKKVVHVFYKGNVLIKDKRCKDEFFHLYTLIVRP 182

RESULT 7  
S29130  
calreticulin (clone 8) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29130; 101068  
R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997; PMID:1445218  
A:Accession: S29130  
A:Molecule type: mRNA  
A:Residues: 1-384 <TR>  
A:Cross-references: EMBL:X67598  
A:Accession: T01068  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-339, 'XTGR' <TR>  
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611  
A:Experimental source: CNS  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:381-384/Region: endoplasmic reticulum retention signal  
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.1%; Score 22; DB 2; Length 384;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLIVRPDNTYEKIDNS 53  
DB 140 FTHLYTLIVRPDNTYEKIDNS 161

RESULT 8  
S29129  
calreticulin precursor (clone 3) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29129  
R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997; PMID:1445218  
A:Accession: S29129  
A:Molecule type: mRNA  
A:Residues: 1-411 <TR>  
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-411/Product: calreticulin #status predicted <MAT>  
F:408-411/Region: endoplasmic reticulum retention signal

F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.1%; Score 22; DB 2; Length 411;  
Best Local Similarity 100.0%; Pred. No. 1.7e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLIVRPDNTYEKIDNS 53  
DB 163 FTHLYTLIVRPDNTYEKIDNS 184

RESULT 9  
S71343  
calreticulin precursor - Korean frog  
C:Species: Rana rugosa (Korean frog)  
C>Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Jun-2000  
C:Accession: S71343  
R:Yamamoto, S.; Nakamura, M.  
FEBS Lett. 387, 27-32, 1996  
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa.  
A:Reference number: S71342; MUID:96234004; PMID:8654561  
A:Accession: S71343  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-419 <YAM>  
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BA11425.1; PID:g1514957  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-119/Product: calreticulin #status predicted <MAT>  
F:205-213/Region: nuclear location signal  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 32.8%; Score 20; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 2.3e-13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 HLYTLIVRPDNTYEKIDNS 53  
DB 171 HLYTLIVRPDNTYEKIDNS 190

RESULT 10  
JH0795  
calreticulin precursor - California sea hare  
N:Alternate names: protein 407  
C:Species: Aplysia californica (California sea hare)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JH0795; B31409; F60977  
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.  
Neuron 9, 1013-1024, 1992  
A:Title: Long-term sensitization training in aplysia leads to an increase in calretic  
A:Reference number: JH0795; MUID:93098937; PMID:1463804  
A:Accession: JH0795  
A:Molecule type: mRNA  
A:Residues: 1-405 <KEN>  
A:Cross-references: GB:S51239; NID:g262053; PIDN:AA824569.1; PID:g262054  
A:Experimental source: abdominal ganglion and anal nervous system  
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988  
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion  
A:Reference number: A94207; MUID:88320566; PMID:3413132  
A:Accession: B31409  
A:Molecule type: protein  
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>  
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,  
Electrophoresis 10, 152-157, 1989  
A:Title: Development of a database of amino acid sequences for proteins identified an  
A:Reference number: A60977; MUID:89276264; PMID:2731514  
A:Accession: F60977  
A:Molecule type: protein  
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>

C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-405/Product: calreticulin #status experimental <MNT>  
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 31.1%; Score 19; DB 1; Length 405;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 HLYTIVRPDNTYEKIDN 52  
Db 166 HLYTIVRPDNTYEKIDN 184

## RESULT 11

A48573  
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)  
C:Species: Schistosoma mansoni  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48573  
R:Khalife, J.; Trotsch, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.  
Mol. Biochem. Parasitol. 57, 193-202, 1993  
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human  
A:Reference number: A48573; MUID:93165070; PMID:8433712  
A:Accession: A48573  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-393 <KHA>  
A:Cross-references: GB:M93097; NID:q160928  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBI:P:125086)  
C:Superfamily: calreticulin  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 23.0%; Score 14; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 5e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TKKVHVFNYKGN 18  
Db 139 TKKVHVFNYKGN 152

## RESULT 12

A56637  
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)  
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog  
C:Species: Drosophila melanogaster  
C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
R:Smith, M.J.  
DNA Seq. 3, 247-250, 1992  
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h  
A:Reference number: A56637; MUID:93208374; PMID:1296819  
A:Accession: A56637  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-406 <SMT>  
A:Cross-references: GB:X64461; NID:97685; PIDN:CAA45791.1; PID:97686  
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sonthelmer, R.D.; Capra, J.D.  
J. Clin. Invest. 86, 332-335, 1990  
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom  
A:Reference number: A37158; MUID:90307981; PMID:2365822  
A:Accession: A37158  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: DNA  
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'U', 185-220 <MCC>  
C:Genetics:  
A:Gene: FlyBase:Crc  
A:Cross-references: FlyBase:FBgn0005585

A:Introns: 65/1; 222/3  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 21.3%; Score 13; DB 2; Length 406;  
Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRPDNTYEY 48  
Db 172 YTLIVRPDNTYEY 184

## RESULT 13

A32507  
41K larval antigen - nematode (Onchocerca volvulus) (fragment)  
C:Species: Onchocerca volvulus  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 12-Apr-1995  
C:Accession: A32507; A28813  
R:Runnisch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.  
J. Clin. Invest. 82, 262-269, 1988  
A:Title: Isolation and characterization of expression cDNA clones encoding antigens o  
A:Reference number: A92769; MUID:88273584; PMID:2455736  
A:Accession: A32507  
A:Molecule type: mRNA  
A:Residues: 1-336 <UNN>  
C:Superfamily: calreticulin

Query Match 19.7%; Score 12; DB 2; Length 336;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVHVIF 12  
Db 83 CGPGTKKVHVIF 94

## RESULT 14

S25851  
calreticulin precursor - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S25851; T33996  
R:Smith, M.J.  
DNA Seq. 2, 235-240, 1992  
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.  
A:Reference number: S25851; MUID:92329978; PMID:1627827  
A:Accession: S25851  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <SMT>  
A:Cross-references: EMBL:X59589; NID:96693; PIDN:CAA42159.1; PID:96694  
R:Baier, C.; Courtney, L.; Laplant, Y.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid Y38A10A.  
A:Reference number: Z21453  
A:Accession: T33996  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-395 <BAN>  
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5  
A:Experimental source: strain Bristol N2; clone Y38A10A  
C:Genetics:  
A:Gene: CESP:Y38A10A.5  
A:Map position: 5  
A:Introns: 107/3; 315/3  
C:Superfamily: calreticulin  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 14.8%; Score 9; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 DNTYEKID 51  
|||||||  
Db 174 DNTYEKID 182

## RESULT 15

A25343  
nonhistone chromosomal protein HMB - Methanosarcina barkeri  
C:Species: Methanosarcina barkeri  
C:Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 16-Feb-1997  
C:Accession: A25343  
R:Laine, B.; Charlier, F.; Imbert, M.; Lewis, R.; Sautiere, P.  
Eur. J. Biochem. 161, 681-687, 1986  
A:Title: Primary structure of the chromosomal protein HMB from the archaeobacteria Methan  
A:Reference number: A25343; MUID:87080318; PMID:3098561  
A:Accession: A25343  
A:Molecule type: protein  
A:Residues: 1-93 <LAI>  
C:Superfamily: methanogen chromosomal protein  
C:Keywords: chromosomal protein; DNA binding

Query Match 11.5%; Score 7; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTKKVHV 10  
|||||||  
Db 51 GTKKVHV 57

Search completed: March 14, 2003, 20:49:00  
Job time : 6.36963 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 2.33047 Seconds  
(without alignments)  
1085.643 Million cell updates/sec

Title: US-09-807-148-5  
Perfect score: 61  
Sequence: 1 CGPCTKKVHVIFNYKKNVL.....PDNTYEVKIDNSQVSSGLE 61

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	416	1	CRTC_MOUSE
2	61	100.0	416	1	CRTC_MOUSE
3	61	100.0	417	1	CRTC_HUMAN
4	61	100.0	418	1	CRTC_MOUSE
5	42	88.9	400	1	CRTL_BOVIN
6	42	88.9	421	1	CRTL_BOVIN
7	14	23.0	393	1	CRTC_BOVINA
8	13	21.3	406	1	CRTC_DROME
9	12	19.7	388	1	RALL_ONCVO
10	12	14.8	395	1	CRTC_CAEEL
11	9	11.5	93	1	HMC1_METRA
12	7	11.5	93	1	HMC1_METRA
13	7	11.5	397	1	RPA2_PYRAB
14	7	11.5	397	1	RPA2_PYRAB
15	7	11.5	397	1	RPA2_PYRAB
16	7	11.5	397	1	RPA2_PYRAB
17	7	11.5	414	1	PKG_SCHPO
18	7	11.5	591	1	CALX_MOUSE
19	7	11.5	591	1	CALX_MOUSE
20	7	11.5	592	1	CALX_MOUSE
21	6	9.8	593	1	CALX_MOUSE
22	6	9.8	62	1	MPK3_XENLA
23	6	9.8	87	1	HMCB_METSO
24	6	9.8	89	1	HMCB_METSO
25	6	9.8	90	1	HMCB_METSO
26	6	9.8	90	1	HMCB_METSO
27	6	9.8	109	1	RLOI_METJA
28	6	9.8	146	1	VAAR_BACSU
29	6	9.8	213	1	HPRT_MOUSE
30	6	9.8	217	1	HPRT_MOUSE
31	6	9.8	217	1	HPRT_MOUSE
32	6	9.8	217	1	HPRT_MOUSE
33	6	9.8	218	1	HPRT_MOUSE

## ALIGNMENTS

RESULT 1	CRTC_MOUSE	STANDARD	PRT	416 AA.
AC	PI4211			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HMCBP) (ERP60).			
GN	CALR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.			
RC	STRAIN-BALB/c; TISSUE=Liver;			
RX	MEDLINE=90059955; PubMed=2583110;			
RA	Smith M.J., Koch G.L.E.;			
RT	"Multiple zones in the sequence of calreticulin (CRP55, calregulin,			
RT	HACBP), a major calcium binding ER/SR protein.";			
RL	EMBO J. 8:3581-3586(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93013037; PubMed=1398135;			
RA	Mazzarella R.A., Gold P., Cunningham M., Green M.;			
RT	"Determination of the sequence of an expressible cDNA clone encoding			
RT	ERP60/calregulin by the use of a novel nested set method.";			
RL	Gene 120:217-225(1992).			
RN	[3]			
RP	SEQUENCE OF 18-38.			
RC	TISSUE=Fibroblast;			
RX	MEDLINE=95009907; PubMed=7523108;			
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;			
RT	"Separation and sequencing of familial and novel murine proteins			
RT	using preparative two-dimensional gel electrophoresis.";			
RL	Electrophoresis 15:735-745(1994).			
CC	-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND			
CC	LOW AFFINITY CALCIUM-BINDING SITES.			
CC	-!- SUBUNIT: MONOMER (BT SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.			
CC	-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
CC	EMBL: X14926; CA33053.1; -			
CC	EMBL: M92988; AA37569.1; -			
CC	PIR: S06763; S06763.			
CC	PIR: JC1444; JC1444.			
CC	SWISS-2DPAGE: PI4211; MOUSE.			
CC	MGD: MGI:88252; Calr.			

DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 416 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 407 ASP/GLU/TYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 413 416 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-56;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKRVHYFVYKNGKLVINKDICKDEFFHLYTLVPRPNTYEVRKIDNSQVSGSL 60  
 DB 137 CGPGTKRVHYFVYKNGKLVINKDICKDEFFHLYTLVPRPNTYEVRKIDNSQVSGSL 196

OY 61 E 61  
 DB 197 E 197

RESULT 2  
 CRTC\_RAT STANDARD; PRT; 416 AA.  
 ID CRTC\_RAT P18418; P10452;  
 AC 01-MAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Calreticulin precursor (CRTC) (Calreticulin) (HACBP) (ERp60) (CALBP)  
 GN CALR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Brain cortex;  
 RX MEDLINE=90370496; PubMed=2395561;  
 RA Murphy K.K., Banville D., Stikant C.B., Carrier F., Bell A.,  
 RA Holmes C., Patel Y.C.;  
 RT "Structural homology between the rat calreticulin gene product and  
 RT the Onchocerca volvulus antigen Ral-1.";  
 RL Nucleic Acids Res. 18:4933-4933(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley;  
 RX MEDLINE=93202172; PubMed=8453984;  
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,  
 RA Okinaga S., Kobayashi T.;  
 RT "An endoplasmic reticulum protein, calreticulin, is transported into  
 RT the acrosome of rat sperm.";

RL Exp. Cell Res. 205:101-110(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;  
 RX MEDLINE=95181573; PubMed=7876339;  
 RA Soenichsen B., Fuehlkrug J., van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Mieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain  
 RT calreticulin in the endoplasmic reticulum.";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 RN [4]  
 RP SEQUENCE OF 270-358 FROM N.A.  
 RC STRAIN-Sprague-Dawley; Latruffe N.;  
 RA Lone Y.C., Bailly A., Latruffe N.;  
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 18-29.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [6]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN-Sprague-Dawley; TISSUE-Testis;  
 RX MEDLINE=92360010; PubMed=1497655;  
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
 RT "Calreticulin is present in the acrosome of spermatozoa of rat  
 RT testis.";  
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
 RN [7]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN-LEC; TISSUE-Liver;  
 RX MEDLINE=94072621; PubMed=8251535;  
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horuchi R.,  
 RA Kametaki T.;  
 RT "Identification of protein disulfide isomerase and calreticulin as  
 RT autoimmune antigens in LEC strain of rats.";  
 RL Biochim. Biophys. Acta 1158:339-344(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-HYDROXYBUTYRATE DEHYDROGENASE.  
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 CC -----  
 DR EMBL: D78308; BAA11345.1; -;  
 DR EMBL: X53363; CAA37446.1; -;  
 DR EMBL: X13702; CAA31987.1; ALT\_SEQ.  
 DR EMBL: X79327; CAA55890.1; -;  
 DR PIR: S04867; S04867.  
 DR PIR: S11205; S11205.  
 DR PIR: S13045; S13045.  
 DR PIR: A49176; A49176.  
 DR PIR: S45036; S45036.  
 DR PIR: JH0819; JH0819.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.

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DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 286713CED31A2970 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGPGKKVHVFNFYNGKAVLNKDKRCDDFTHTLTLPDNTYEKIDNSQVSGSL 60
Db 137 CGPGKKVHVFNFYNGKAVLNKDKRCDDFTHTLTLPDNTYEKIDNSQVSGSL 196

Oy 61 E 61
Db 197 E 197

RESULT 3
CRTC_HUMAN STANDARD: PRT: 417 AA.
AC P27797;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HMCBP) (ERP60).
GN CALR OR CRTC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013129; PubMed=1919005;
RA Rokeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.;
RT "Characterization of the autoantigen calreticulin.";
RL J. Immunol. 147:3031-3039(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237213; PubMed=2332496;
RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92129342; PubMed=1733953;
RA McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]

RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCready P., Stiliagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [7]
RP SEQUENCE OF 18-36.
RX MEDLINE=92002034; PubMed=1911778;
RA Kojani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866(1991).
RN [8]
RP SEQUENCE OF 18-32.
RX MEDLINE=90380058; PubMed=2400400;
RA Krause K.H., Simeerman H.K.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RL Biochem. J. 270:545-548(1990).
RN [9]
RP SEQUENCE OF 18-28.
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargias R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [10]
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., Van Damme J., Puyse M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [11]
RP SEQUENCE OF 18-26.
RX TISSUE-Colon carcinoma;
RA MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
RN [12]
RP FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
RP LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
CC autoantigen.
CC
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CC EMBL; M84739; AAA51916.1; -
CC EMBL; M32294; AAA36582.1; -
CC EMBL; AY047586; AAL13126.1; -

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FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DISULFID 351 408 ASP/GLU/LYS-RICH.
FT DOMAIN 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MM; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHIFNYKGNVINKDIRCKDDEFTHTLTVRPDNTYEKINDNSQVESGL 60
DB 137 CGPGTKKVVHIFNYKGNVINKDIRCKDDEFTHTLTVRPDNTYEKINDNSQVESGL 196

QY 61 E 61
DB 197 E 197

RESULT 5
CRT1_BOVIN
ID CRT1_BOVIN STANDARD: PRT: 400 AA.
AC P52193:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE-Brain;
RC MEDLINE=94183174; PubMed=8135753;
RA Matsuda K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.
FT CHAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.

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FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146 N-LINKED (GLCNAC. . .).
FT CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 MM; 7DAB6BDFC689EF1 CRC64;

Query Match 68.9%; Score 42; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.3e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHIFNYKGNVINKDIRCKDDEFTHTLTVRP 42
DB 120 CGPGTKKVVHIFNYKGNVINKDIRCKDDEFTHTLTVRP 161

RESULT 6
CRT2_BOVIN
ID CRT2_BOVIN STANDARD: PRT: 421 AA.
AC P42818:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE-Brain;
RC MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC
DR EMBL: L13462; AAC37307.1; .
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.

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FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 195 206 1-1.
FT REPEAT 214 225 1-2.
FT REPEAT 231 242 1-3.
FT REPEAT 248 259 1-4.
FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA: 48812 MW: 0257E959F71528BC CRC64;

Query Match 68.9%; Score 42; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.3e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLYTVLRP 42
DB 141 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLYTVLRP 182

RESULT 7
CRTC_SCHMA STANDARD; PRT; 393 AA.
ID CRTC_SCHMA 006814; 026562;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calreticulin precursor (SM4 protein).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=93165070; PubMed=8433712;
RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,
RA Capron A.;
RT "Cloning of the gene encoding a Schistosoma mansoni antigen
RT homologous to human Ro/SS-A autoantigen."
RL Mol. Biochem. Parasitol. 57:193-202(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=94187805; PubMed=8139623;
RA Khalife J., Pierce R.J., Godin C., Capron A.;
RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
RT calreticulin."
RL Mol. Biochem. Parasitol. 62:313-315(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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DR EMBL: M93097; AAA29854.1; -
DR EMBL: U24159; AAA19024.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.

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DR PROSITE: PS00014; ER_TARGET.1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal; Glycoprotein.
FT SIGNAL 1 16
FT CHAIN 17 393 CALRETICULIN.
FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 209 220 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 243 254 1-4.
FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 135 161 BY SIMILARITY.
FT SITE 390 393 PREVENT SECRETION FROM ER.
FT CONFLICT 89 90 MY -> IL (IN REF. 2).
FT CONFLICT 188 207 MISSING (IN REF. 2).
FT CONFLICT 378 378 Y -> D (IN REF. 2).
SQ SEQUENCE 393 AA: 45397 MW: 45F59857C21940D2 CRC64;

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OY 5 TKKVHVIFNYKGN 18
DB 139 TKKVHVIFNYKGN 152

RESULT 8
CRTC_DROME STANDARD; PRT; 406 AA.
ID CRTC_DROME P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).
GN Drosophila melanogaster (Fruit fly).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue."
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise J.R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Meherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostreft A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclele J.M.,  
RA Palazszo L., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*";  
RL Science 287:2185-2195(2000).  
RN [3]  
RP SEQUENCE OF 91-124 AND 182-220.  
RX MEDLINE=90307981; PubMed=2365822;  
RA McCauliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,  
RA Capra J.D.;  
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
RT highly homologous with onchocercal RAL-1 antigen and an alysia  
RT 'memory molecule'";  
RL J. Clin. Invest. 86:332-335(1990).  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
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CC -----  
CC EMBL; X64461; CAA45791.1; -;  
DR EMBL; AE003683; AA5416.1; -;  
DR PIR; A37158; A37158.  
DR FlyBase; FBgn0005585; Crc.  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER\_target.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; CALRETICULIN; 1.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 406 POTENTIAL.  
FT CONFLICT 107 107 G -> A (IN REF. 3).  
FT CONFLICT 184 184 V -> L (IN REF. 3).  
FT SEQUENCE 406 AA; 46808 MW; 65D72C69D0BC427 CRC64;  
Query Match 21.3%; Score 13; DB 1; Length 406;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
RALL1\_ONCVO  
ID RALL1\_ONCVO STANDARD: PRT; 388 AA.  
AC P11012;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE RAL-1 protein precursor (41 kDa larval antigen).  
GN RAL1.  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94341871; PubMed=7520419;  
RA Rokeach L.A., Zimmerman P.A., Unasch T.R.;  
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the  
RT calreticulin family of proteins, recognized by sera from patients  
RT with onchocerciasis";  
RL Infect. Immun. 62:3696-3704(1994).  
RN [2]  
RP SEQUENCE OF 53-388 FROM N.A.  
RX MEDLINE=88273584; PubMed=2455736;  
RA Unasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;  
RT "Isolation and characterization of expression cDNA clones encoding  
RT antigens of Onchocerca volvulus infective larvae";  
RL J. Clin. Invest. 82:262-269(1988).  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
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CC -----  
CC EMBL; M20565; AA59056.1; -;  
DR PIR; A32507; A32507.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; CALRETICULIN; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Calcium-binding; Repeat; Antigen; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 388 RAL-1 PROTEIN.  
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
FT REPEAT 189 200 1-1.  
FT REPEAT 208 219 1-2.  
FT REPEAT 225 236 1-3.  
FT REPEAT 242 253 1-4.  
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
FT REPEAT 257 267 2-1.  
FT REPEAT 271 281 2-2.  
FT REPEAT 285 295 2-3.  
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
FT DISULFID 135 161 BY SIMILARITY.  
FT SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;  
Query Match 19.7%; Score 12; DB 1; Length 388;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
 CRIC\_CAEEL STANDARD; PRT; 395 AA.  
 AC P27798;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Calreticulin precursor.  
 GN CRT-1 OR Y38A10A.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RX MEDLINE=9232978; PubMed=1627827;  
 RA Smith M.J.;  
 RT "A.C. elegans gene encodes a protein homologous to mammalian  
 calreticulin."  
 RL DNA Seq. 2:235-240(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Bauer C., Courtney L., Laplant Y.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RP REVISIONS.  
 RA Waterston R.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X59589; CAA42159.1; -;  
 DR EMBL; AF125963; AAD14746.1; -;  
 DR PIR; S25851; S25851.  
 DR Wormpep; Y38A10A.5; CE21562.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; Calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
 FT SIGNAL 1 15  
 FT CHAIN 16 395  
 FT DOMAIN ? 192  
 FT DOMAIN 193 301  
 FT DOMAIN 302 395  
 FT DOMAIN 186 250  
 FT REPEAT 186 197  
 FT REPEAT 205 216  
 FT REPEAT 222 233  
 FT REPEAT 239 250  
 FT DOMAIN 254 292  
 FT REPEAT 254 264  
 FT REPEAT 264 278  
 FT REPEAT 282 292  
 FT DOMAIN 332 390  
 FT DISULFID 133 158

FT SITE 392 395 PREVENT SECRETION FROM ER.  
 SO SEQUENCE 395 AA; 45616 MW; 35CA7D2E61D56B03 CRC64;  
 Query Match 14.8%; Score 9; DB 1; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 0.044;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 43 DNTYEKID 51  
 DB 174 DNTYEKID 182  
 RESULT 11  
 HMCL\_METTE STANDARD; PRT; 93 AA.  
 ID HMCL\_METTE  
 AC P06116;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-AUG-1990 (Rel. 15, Last annotation update)  
 DE Chromosomal protein MCI (HMB).  
 OS Methanosarcina barkeri.  
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2208;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-MS / DSM 800;  
 RX MEDLINE=87080318; PubMed=3098561;  
 RA Laine B., Chartier F., Imbert M., Lewis R., Sautiere P.;  
 RT "Primary structure of the chromosomal protein HMB from the  
 archaeobacteria Methanosarcina barkeri."  
 RL Eur. J. Biochem. 161:681-687(1986).  
 RN [2]  
 RP CONFORMATIONAL STUDIES.  
 RX MEDLINE=90254162; PubMed=2111171;  
 RA Imbert M., Laine B., Helbecque N., Mornon J.-P., Henchart J.-P.,  
 Sautiere P.;  
 RT "Conformational study of the chromosomal protein MCI from the  
 archaeobacterium Methanosarcina barkeri."  
 RL Biochim. Biophys. Acta 1038:346-354(1990).  
 CC -1- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES  
 TRANSCRIPTION.  
 CC PIR; A25343; A25343.  
 DR PIR; S13716; S13716.  
 DR KW DNA-binding.  
 SQ SEQUENCE 93 AA; 10755 MW; 3B5E17405CE2171C CRC64;  
 Query Match 11.5%; Score 7; DB 1; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 GTRKVVH 10  
 DB 51 GTRKVVH 57  
 RESULT 12  
 HMCL\_METTE STANDARD; PRT; 93 AA.  
 ID HMCL\_METTE  
 AC P12770;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-AUG-1990 (Rel. 15, Last annotation update)  
 DE Chromosomal protein MCI.  
 OS Methanosarcina thermophila.  
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2210;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-CHTI 55 / DSM 2902;  
 RX MEDLINE=89335731; PubMed=2503033;  
 RA Chartier F., Laine B., Belaitche D., Touzel J.-P., Sautiere P.;

RT "Primary structure of the chromosomal protein MCI from the  
RT archaebacterium Methanosarcina sp. CHTI 55.";  
RL Biochim. Biophys. Acta 1008:309-314(1989).  
CC -I- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES  
CC TRANSCRIPTION.  
DR PIR: S05243; S05243.  
DR PIR: S13712; S13712.  
KW DNA-binding.  
SQ SEQUENCE 93 AA; 10663 MW; 294AA187BD549C28 CRC64;

Query Match 11.5%; Score 7; DB 1; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GTKKVHV 10  
Db 51 GTKKVHV 57

RESULT 13  
RPA2\_PYRAB STANDARD; PRT; 397 AA.  
AC 09Y113;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).  
GN RPOA2 OR PAB0425.  
OS Pyrococcus abyssi.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=29292;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GES / Orsay;  
RA Heilig R.;  
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
RT structure and evolution.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
CC SUBSTRATES.  
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC (RNA)(N).  
CC -I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
CC -----  
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CC -----  
DR EMBL: AJ248284; CAB49538.1; .  
DR InterPro: IPR002879; RNA\_pol\_A2.  
DR Pfam: PF01854; RNA\_pol\_A2; 1.  
KW Transferase; Transcription; DNA-directed RNA polymerase;  
KW Complete proteome.  
SQ SEQUENCE 397 AA; 44594 MW; E459658EAE9C15CB CRC64;

Query Match 11.5%; Score 7; DB 1; Length 397;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRP 42  
Db 198 YTLIVRP 204

RESULT 14  
RPA2\_PYRFU STANDARD; PRT; 397 AA.

AC Q80UM5;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).  
GN RPOA2 OR PFI562.  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;  
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;  
RT "The complete sequence of the Pyrococcus furiosus genome.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
CC -I- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription  
CC of DNA into RNA using the four ribonucleoside triphosphates as  
CC substrates.  
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC (RNA)(N).  
CC -I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
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CC -----  
DR EMBL: AE010257; AAL81686.1; .  
DR Transferase; Transcription; DNA-directed RNA polymerase;  
KW Complete proteome.  
SQ SEQUENCE 397 AA; 44404 MW; 19D46E356CA0E49F CRC64;

Query Match 11.5%; Score 7; DB 1; Length 397;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRP 42  
Db 198 YTLIVRP 204

RESULT 15  
RPA2\_PYRHO STANDARD; PRT; 397 AA.  
AC 09J777;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).  
GN RPOA2 OR PHI544.  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OT3;  
RA MEDLINE=98344137; PubMed=9679194;  
RA Kawaiibayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Ogunchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuchi Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-  
RT thermophilic archaebacterium, Pyrococcus horikoshii OT3.";  
RL DNA Res. 5:55-76(1998).  
CC -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

```
CC SUBSTRATES.
CC -I CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(N).
CC -I SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----
CC DR EMBL; AP000006; BAA30655.1; -
CC DR InterPro; IPR002879; RNA_POL_A2.
CC DR Pfam; PF01854; RNA_POL_A2; 1.
CC KW Transferase; Transcription; DNA-directed RNA polymerase;
CC KW Complete proteome.
CC SO SEQUENCE 397 AA; 44507 MW; 7846655AB5D4730D CRC64;

QY 36 YTLIVRP 42
   |||||
Db 198 YTLIVRP 204
```

Search completed: March 14, 2003, 20:45:07  
Job time : 4.33047 secs



OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=CNS;  
 RA Treves S., Zorzato F., Pozzan T.;  
 RT "Identification of calreticulin isoform in the CNS."  
 RL Biochem. J. 0:0-0(0).  
 DR EMBL: X67598; CAA47867.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER  
 SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 36.1%; Score 22; DB 13; Length 343;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLIVRPDNTYEKIDNS 53  
 DB 140 FTHLYTLIVRPDNTYEKIDNS 161

RESULT 3  
 ID 091710 PRELIMINARY; PRT; 411 AA.  
 AC 091710;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin precursor (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=CNS;  
 RA Treves S., Zorzato F., Pozzan T.;  
 RT "Identification of calreticulin isoform in the CNS."  
 RL Biochem. J. 0:0-0(0).  
 DR EMBL: X67597; CAA47866.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
 FT NON\_TER  
 SQ SEQUENCE 411 AA; 48344 MW; 891DA66E00EBEFA CRC64;

Query Match 36.1%; Score 22; DB 13; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLIVRPDNTYEKIDNS 53  
 DB 163 FTHLYTLIVRPDNTYEKIDNS 184

RESULT 4  
 ID 098984 PRELIMINARY; PRT; 419 AA.  
 AC 098984;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin.  
 OS Rana rugosa (wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96234004; PubMed=8654561;  
 RA Yamamoto S., Nakamura M.;  
 RT "Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa."  
 RL FEBS Lett. 387:27-32(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;  
 RT "Strong expression of the calreticulin gene in the liver of Rana rugosa tadpoles, but not adult frogs."  
 RL J. Exp. Zool. 275:431-443(1996).  
 DR EMBL: D78589; BAA11425.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER  
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 32.8%; Score 20; DB 13; Length 419;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 HLYTLIVRPDNTYEKIDNS 53  
 DB 171 HLYTLIVRPDNTYEKIDNS 190

RESULT 5  
 ID 026268 PRELIMINARY; PRT; 405 AA.  
 AC 026268;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=93098937; PubMed=1463604;  
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein."  
 RL Neuron 9:1013-1024(1992).  
 DR EMBL: S51239; AAB24569.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin.1.



DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; CALRETICULIN.1.  
DR PROSITE: PS00803; CALRETICULIN.1; 1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DID69 CRC64;

Query Match 31.1%; Score 19; DB 5; Length 405;  
Best Local Similarity 100.0%; Pred. No. 1.7e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 HLYTLVPRDNTYEKIDN 52  
|||||  
DB 166 HLYTLVPRDNTYEKIDN 164

## RESULT 6

O9PTX7 PRELIMINARY; PRT; 318 AA.  
AC O9PTX7: PRELIMINARY; PRT; 318 AA.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin (Fragment).  
OS Lehteneron reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzonidae; Lethenteron.  
OX NCBI\_TaxID=7753;  
RN [1]

RP MEDLINE-20063780; PubMed-10594174;  
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
RT genes";  
RL J. Mol. Evol. 49:729-735(1999).  
DR EMBL: AB025328; BAA88481.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin.1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; CALRETICULIN.1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
FT NON\_TER 1  
SQ SEQUENCE 318 AA; 36997 MW; C88102EALCAC1506 CRC64;

Query Match 29.5%; Score 18; DB 13; Length 318;  
Best Local Similarity 100.0%; Pred. No. 1.7e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHIFNYKGN 18  
|||||  
DB 36 CGPGTKKVVHIFNYKGN 53

## RESULT 7

O16893 PRELIMINARY; PRT; 410 AA.  
AC O16893:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Calreticulin.  
GN CRT-1.  
OS Amblyomma americanum.  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Parasitiformes; Ixodidae; Ixodidae; Amblyomma.  
OX NCBI\_TaxID=6943;  
RN [1]  
RP SEQUENCE OF 49-410 FROM N.A.  
RC TISSUE-SALIVARY GLANDS;

RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,  
RA Needham G.R.;  
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
RT saliva";  
RL J. Insect Physiol. 41:369-375(1995).  
RN [2]

RC SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLANDS;  
RA Jaworski D.C.;  
RL Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.  
RN [3]

RP SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLANDS;  
RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;  
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: U07708; AAC79094.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin.1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; CALRETICULIN.1.  
DR PROSITE: PS00803; CALRETICULIN.1; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 29.5%; Score 18; DB 5; Length 410;  
Best Local Similarity 100.0%; Pred. No. 2.1e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHIFNYKGN 18  
|||||  
DB 136 CGPGTKKVVHIFNYKGN 153

## RESULT 8

O9U6S0 PRELIMINARY; PRT; 421 AA.  
AC O9U6S0:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Calreticulin precursor.  
GN CALRET.  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinozoa; Echinozoa; Echinodermata; Echinozoa; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Susan J.M., Just M.L., Lennarz W.J.;  
RT "Cloning and Characterization of Alpha Integrin and Calreticulin in  
RT Embryos of the Sea Urchin";  
RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF17915; AAD55725.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin.1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; CALRETICULIN.1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
FT SIGNAL  
FT CHAIN 1 19 POTENTIAL.  
FT CHAIN 20 421 CALRETICULIN.

Query Match 29.5%; Score 18; DB 5; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.1e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKHVIFNYKGN 18  
DB 136 CGPGTKHVIFNYKGN 153

## RESULT 9

O9UDG2 PRELIMINARY; PRT; 214 AA.

AC 09UDG2; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
DE 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
OS CALRETICULIN-CALCIUM binding protein (Fragments).  
OC Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95143082; PubMed=7841019;  
RA Houten G., Koch C.;  
RT "Human placental calreticulin: purification, characterization and  
association with other proteins."  
RL Acta Chem. Scand. 48:905-911(1994).  
DR InterPro: IPR001580; Calreticulin.  
DR Prodom: PD001866; Calreticulin; 1.  
FT NON\_TER 1  
FT NON\_CONS 31 32  
FT NON\_CONS 59 60  
FT NON\_CONS 78 79  
FT NON\_CONS 116 117  
FT NON\_TER 214  
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 23.0%; Score 14; DB 4; Length 214;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 VKINDSVEGSLE 61  
DB 95 VKINDSVEGSLE 108

## RESULT 10

O967Z2 PRELIMINARY; PRT; 395 AA.

AC 0967Z2; 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
DE 01-MAR-2002 (TREMBlrel. 20, last annotation update)  
OS Calcium binding protein calreticulin precursor.  
OC Taenia solium.  
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
OC Cyclophyllidae; Taeniidae; Taenia.  
OX NCBI\_Taxid=6204;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mendlovic F., Ostoa-Saloma P., Flisser A., Lachette J.P.;  
RT "Molecular characterization of Taenia solium calreticulin."  
RL Submitted (Jan-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF340232; AAK52725.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR Prodom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; UNKNOWN\_1.  
DR PROSITE: PS00804; CALRETICULIN\_2; UNKNOWN\_1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; UNKNOWN\_1.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
RN Signal.  
FT SIGNAL 1 18 POTENTIAL.  
SQ SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;

Query Match 21.3%; Score 13; DB 5; Length 395;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 THLYTVRPDNT 45  
DB 168 THLYTVRPDNT 180

## RESULT 11

O9U916 PRELIMINARY; PRT; 406 AA.

AC 09U916; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
OS CALRETICULIN.  
GN CRC OR CG9429.  
OC Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OREGON-R;  
RA Dodo K., Sakoyama Y., Gamo S.;  
RT "Drosophila melanogaster calreticulin for mRNA."  
RL Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AB000718; BA85379.1; -;  
DR Flybase: FBgn005585; Crc.  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR Prodom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 21.3%; Score 13; DB 5; Length 406;  
Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRPDNTYEV 48  
DB 172 YTLIVRPDNTYEV 184

## RESULT 12

O26514 PRELIMINARY; PRT; 350 AA.

AC 026514; 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
OS CALRETICULIN (Fragment).  
GN RAL-1.  
OC Schistosoma japonicum (blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_Taxid=6182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHINESE;  
RA Huggins M.C., Moloney N.A.;  
RT "Cloning of a gene encoding a Schistosoma japonicum vaccine candidate  
with homology to a human Ro/SS-A autoantigen."  
RL Submitted (Aug-1993) to the EMBL/Genbank/DBJ databases.  
DR EMBL: M80524; AAA29917.1; -;  
DR InterPro: IPR001580; Calreticulin.

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DR InterPro: IPR000886; ER_target.  
DR Pfam: PF00626; Calreticulin; 1.  
DR PRINTS: PR001866; Calreticulin; 1.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN_1; 1.  
DR PROSITE: PS00804; CALRETICULIN_2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.  
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.  
FT NON_TER 1  
SQ SEQUENCE 350 AA: 40385 MW: 30FABA4EBB685D1C CRC64;  
  
Query Match 19.7%; Score 12; DB 5; Length 350;  
Best Local Similarity 100.0%; Pred. No. 6.7e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 33 THLYTLIVRPD 44  
DB 122 THLYTLIVRPD 133  
|||||  
  
RESULT 13  
ID 018478 PRELIMINARY; PRT; 375 AA.  
AC 018478;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE RAL-1 protein (Fragment).  
OS Litomosoides sigmodontis.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Litomosoides.  
OX NCBI_TaxID=42156;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Maclean K., Hoffman W.H., Taylor D.W.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ001621; CA04877.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN_1; 1.  
DR PROSITE: PS00804; CALRETICULIN_2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.  
FT NON_TER 375  
SQ SEQUENCE 375 AA: 43842 MW: 03F7642FBF7A5B8 CRC64;  
  
Query Match 19.7%; Score 12; DB 5; Length 375;  
Best Local Similarity 100.0%; Pred. No. 7.1e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGPGTKVHVIF 12  
DB 135 CGPGTKVHVIF 146  
|||||  
  
RESULT 14  
ID 097372 PRELIMINARY; PRT; 387 AA.  
AC 097372;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Calreticulin precursor.  
OS Dirofilaria immitis (Canine heartworm).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Dirofilaria.  
OX NCBI_TaxID=6287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-99094497; PubMed-9879888;  
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.;  
RT "Molecular characterization of a calcium-binding protein from the
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RT filarial parasite Dirofilaria immitis.";  
RL Mol. Biochem. Parasitol. 97:69-79(1998).  
DR EMBL: AF052978; AA03405.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN_1; 1.  
DR PROSITE: PS00804; CALRETICULIN_2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.  
KW Signal.  
FT SIGNAL 1  
FT CHAIN 19 387 POTENTIAL.  
SQ SEQUENCE 387 AA: 44941 MW: E7741BF6AFA5885 CRC64;  
  
Query Match 19.7%; Score 12; DB 5; Length 387;  
Best Local Similarity 100.0%; Pred. No. 7.3e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGPGTKVHVIF 12  
DB 135 CGPGTKVHVIF 146  
|||||  
  
RESULT 15  
ID 045034 PRELIMINARY; PRT; 396 AA.  
AC 045034;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin.  
OS Schistosoma japonicum (blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiidae;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI_TaxID=6182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PHILIPPINE;  
RX MEDLINE-21165812; PubMed-11269324;  
RT Scott J.C., McManus D.P.;  
RT "Molecular cloning and functional expression of a cDNA encoding the  
RT major endoplasmic reticulum-associated calcium-binding protein,  
RT calreticulin, from Philippine strain Schistosoma japonicum.";  
RL Parasitol. Int. 48:35-46(1999).  
DR EMBL: AF044408; AAC00515.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN_1; 1.  
DR PROSITE: PS00804; CALRETICULIN_2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.  
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.  
SQ SEQUENCE 396 AA: 45814 MW: C57394C6FB4CD77B CRC64;  
  
Query Match 19.7%; Score 12; DB 5; Length 396;  
Best Local Similarity 100.0%; Pred. No. 7.5e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 33 THLYTLIVRPD 44  
DB 168 THLYTLIVRPD 179  
|||||  
  
Search completed: March 14, 2003, 20:47:38  
Job time : 10.1566 secs
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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 3.43744 Seconds  
(without alignments)  
522.132 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 61

Sequence: 1 CGPGTKKVVHIFNVKGNVL.....PDNTRYEVKIDNSQVESGSL 61

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCFUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	11.5	593	1	US-08-296-362-2
2	7	11.5	1009	4	US-09-603-146-4
3	6	9.8	69	4	US-09-134-001C-5362
4	6	9.8	74	4	US-09-134-001C-4815
5	6	9.8	94	4	US-09-134-001C-5410
6	6	9.8	184	3	US-08-630-172-2
7	6	9.8	184	4	US-09-375-419-2
8	6	9.8	185	4	US-09-384-162-11
9	6	9.8	218	1	US-08-644-664B-14
10	6	9.8	218	2	US-08-761-277A-14
11	6	9.8	318	1	US-08-530-950-2
12	6	9.8	318	1	US-08-446-083-2
13	6	9.8	318	4	US-08-888-429A-2
14	6	9.8	318	4	US-09-149-879-2
15	6	9.8	351	4	US-08-466-465-6
16	6	9.8	418	3	US-08-630-172-18
17	6	9.8	418	4	US-09-375-419-18
18	6	9.8	504	4	US-09-499-302A-6
19	6	9.8	512	2	US-08-557-122A-33
20	6	9.8	512	4	US-09-262-666-33
21	6	9.8	812	1	US-08-446-794A-4
22	6	9.8	891	4	US-09-134-001C-4913
23	5	8.2	6	4	US-08-874-197-3
24	5	8.2	6	4	US-08-874-197-7
25	5	8.2	6	4	US-08-648-182-3
26	5	8.2	6	4	US-08-648-182-7
27	5	8.2	10	1	US-08-594-447-12

28	5	8.2	10	1	US-08-541-964-11	Sequence 11, Appl
29	5	8.2	10	2	US-08-665-647-26	Sequence 26, Appl
30	5	8.2	12	1	US-08-446-856A-10	Sequence 10, Appl
31	5	8.2	12	1	US-08-446-856A-11	Sequence 11, Appl
32	5	8.2	15	2	US-08-447-411-64	Sequence 64, Appl
33	5	8.2	15	2	US-08-662-227-21	Sequence 21, Appl
34	5	8.2	15	2	US-08-662-227-22	Sequence 22, Appl
35	5	8.2	15	4	US-09-017-947-21	Sequence 21, Appl
36	5	8.2	15	4	US-09-017-947-22	Sequence 22, Appl
37	5	8.2	20	3	US-08-467-023-38	Sequence 38, Appl
38	5	8.2	20	3	US-08-467-023-39	Sequence 39, Appl
39	5	8.2	22	3	US-09-024-020B-18	Sequence 18, Appl
40	5	8.2	22	4	US-09-425-043-18	Sequence 18, Appl
41	5	8.2	24	1	US-08-484-635-111	Sequence 111, App
42	5	8.2	24	2	US-08-484-631-111	Sequence 111, App
43	5	8.2	24	2	US-08-827-570-111	Sequence 111, App
44	5	8.2	31	1	US-08-248-021A-4	Sequence 4, Appl
45	5	8.2	32	1	US-08-248-021A-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-08-296-362-2  
; Sequence 2, Application US/08296362  
; Patent No. 5691306  
; GENERAL INFORMATION:  
; APPLICANT: Bergeron, John J.M.  
; APPLICANT: Thomas, David Y.  
; APPLICANT: Wada, Ikuo  
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF  
; TITLE OF INVENTION: PROTEIN TRAFICKING DISORDERS AND INCREASING SECRETORY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/296,362  
; FILING DATE: 25-AUG-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deehr, Manya S.  
; REGISTRATION NUMBER: 37,120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682-6031  
; TELEFAX: 3723836  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 593 amino acids  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-296-362-2  
Query Match 11.5%, Score 7, DB 1: Length 593;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
33 THLYTLI 39  
|||||||

Db 236 THLYTLI 242

RESULT 2  
US-09-693-146-4  
; Sequence 4, Application US/09693146  
; Patent No. 6413758  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Shuang-yong  
; APPLICANT: Zhu, Zhenyu  
; APPLICANT: Xiao, Jian-ping  
; TITLE OF INVENTION: Method For Cloning And Expression Of Bpmi Restriction  
; TITLE OF INVENTION: Endonuclease In E. coli  
; FILE REFERENCE: NEB-183  
; CURRENT APPLICATION NUMBER: US/09/693,146  
; CURRENT FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1009  
; TYPE: PRT  
; ORGANISM: Bacillus pumilus  
US-09-693-146-4

Query Match  
Best Local Similarity 11.5%; Score 7; DB 4; Length 1009;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IFNYKK 17  
|||||  
Db 741 IFNYKK 747

RESULT 3  
US-09-134-001C-5362  
; Sequence 5362, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5362  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5362

Query Match  
Best Local Similarity 9.8%; Score 6; DB 4; Length 69;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23  
|||||  
Db 29 NVLINK 34

RESULT 4  
US-09-134-001C-4815  
; Sequence 4815, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4815  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4815

Query Match  
Best Local Similarity 9.8%; Score 6; DB 4; Length 74;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 HLYTLI 39  
|||||  
Db 15 HLYTLI 20

RESULT 5  
US-09-134-001C-5410  
; Sequence 5410, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5410  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5410

Query Match  
Best Local Similarity 9.8%; Score 6; DB 4; Length 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23  
|||||  
Db 21 NVLINK 26

RESULT 6  
US-08-630-172-2  
; Sequence 2, Application US/08630172  
; Patent No. 6060054  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-2

Query Match 9.8%; Score 6; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KGNVL 20  
|||||  
DB 89 KGNVL 94

RESULT 7  
US-09-375-419-2  
Sequence 2, Application US/09375419  
Patent No. 6264950

GENERAL INFORMATION:  
APPLICANT: Staerz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
TITLE OF INVENTION: LYMPHOCYTE VETO  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/375,419  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,172

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-09-375-419-2

Query Match 9.8%; Score 6; DB 4; Length 184;

Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KGNVL 20  
|||||  
DB 89 KGNVL 94

RESULT 8  
US-09-384-162-11

Sequence 11, Application US/09384162  
Patent No. 6376747

GENERAL INFORMATION:  
APPLICANT: Xing, Ti  
APPLICANT: Malik, Kamal  
APPLICANT: Martin-Heller, Teresa  
APPLICANT: Miki L., Brian  
TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase  
FILE REFERENCE: 08-884280US  
CURRENT APPLICATION NUMBER: US/09/384,162  
CURRENT FILING DATE: 1999-08-27  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 11  
LENGTH: 185  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-384-162-11

Query Match 9.8%; Score 6; DB 4; Length 185;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23  
|||||  
DB 108 NVLINK 113

RESULT 9  
US-08-644-664B-14

Sequence 14, Application US/08644664B  
Patent No. 5776746

GENERAL INFORMATION:  
APPLICANT: Denney Jr., Dan W.  
TITLE OF INVENTION: Gene Amplification Methods  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/644,664B  
FILING DATE: 01-MAY-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: GENIPOPE-00912

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-644-664B-14

Query Match 9.8%; Score 6; DB 1; Length 218;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GKNVLI 21  
|||||  
DB 127 GKNVLI 132

RESULT 10  
US-08-761-277A-14  
; Sequence 14, Application US/08761277A  
; Patent No. 5972334  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/761,277A  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/644,664  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Macknight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: GENITOPE-02406  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ. ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-761-277A-14

Query Match 9.8%; Score 6; DB 2; Length 218;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GKNVLI 21  
|||||  
DB 127 GKNVLI 132

RESULT 11  
US-08-530-950-2  
; Sequence 2, Application US/08530950  
; Patent No. 5736381  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Roger J.  
; APPLICANT: Rainsaud, Joel  
; APPLICANT: Gupta, Shashi

APPLICANT: Derjard, Benoit  
; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
; TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/530,950  
; FILING DATE: 19-SEP-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fasse, J. Peter  
; REGISTRATION NUMBER: 32,983  
; REFERENCE/DOCKET NUMBER: 07917/010001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154

INFORMATION FOR SEQ. ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 318 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
US-08-530-950-2

Query Match 9.8%; Score 6; DB 1; Length 318;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23  
|||||  
DB 166 NVLINK 171

RESULT 12  
US-08-446-083-2  
; Sequence 2, Application US/08446083  
; Patent No. 5804427  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Roger J.  
; APPLICANT: Rainsaud, Joel  
; APPLICANT: Gupta, Shashi

APPLICANT: Derjard, Benoit  
; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
; TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,083



FILING DATE: 19-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 04020/066001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-446-083-2

Query Match 9.8%; Score 6; DB 1; Length 318;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 NVLINK 23  
111111  
Db 166 NVLINK 171

RESULT 13  
US-08-888-429A-2  
Sequence 2, Application US/0888429A  
Patent No. 6136596  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Whitmarsh, Alan  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, Peter J.  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 299354  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

FRAGMENT TYPE: internal  
US-08-888-429A-2

Query Match 9.8%; Score 6; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 NVLINK 23  
111111  
Db 166 NVLINK 171

RESULT 14  
US-09-149-879-2  
Sequence 2, Application US/09149879  
Patent No. 6174676  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Raingeaud, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Deljard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/149,879  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
US-09-149-879-2

Query Match 9.8%; Score 6; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 NVLINK 23  
111111  
Db 166 NVLINK 171

RESULT 15  
US-08-466-465-6  
Sequence 6, Application US/08466465  
Patent No. 6162432

GENERAL INFORMATION:  
APPLICANT: Wallner, Barbara P.  
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen  
TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using  
TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,465  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/08755  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/862,022  
FILING DATE: 12-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/770,969  
FILING DATE: 07-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis (PLM)  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: BGP-111CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-466-465-6

Query Match 9.8%; Score 6; DB 4; Length 351;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KGKNVL 20  
|||||  
DB 113 KGKNVL 118

Search completed: March 14, 2003, 20:50:08  
Job time : 5.43744 secs

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 2.97135 Seconds  
(without alignments)  
946.243 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 61

Sequence: 1 CGPGTKKVVHVFENYKGNVL.....PDNTYEKIDNSQVSSGL 61

## Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCr\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	417	9	US-09-906-393A-36
2	12	19.7	112	9	US-09-906-393A-6
3	6	9.8	116	9	US-10-078-770-118
4	6	9.8	125	9	US-10-078-770-132
5	6	9.8	218	9	US-09-925-664-14
6	6	9.8	218	10	US-09-189-833B-7
7	6	9.8	218	10	US-09-189-833B-8
8	6	9.8	218	10	US-09-902-705-7
9	6	9.8	218	10	US-09-902-705-8
10	6	9.8	226	9	US-09-895-913A-362
11	6	9.8	247	10	US-09-815-242-11342
12	6	9.8	247	10	US-09-815-242-11342
13	6	9.8	250	12	US-10-062-254-90
14	6	9.8	289	10	US-10-062-254-90
15	6	9.8	295	10	US-09-815-242-11836
16	6	9.8	312	9	US-09-815-242-11836
17	6	9.8	318	9	US-09-966-459A-10
18	6	9.8	351	10	US-09-761-569-2
19	6	9.8	351	10	US-09-796-033-6
					US-09-730-465-6

20	6	9.8	411	9	US-10-002-050-10	Sequence 10, Appl
21	6	9.8	411	9	US-10-002-304-10	Sequence 10, Appl
22	6	9.8	411	12	US-10-003-152-10	Sequence 10, Appl
23	6	9.8	423	10	US-09-728-674-160	Sequence 160, App
24	6	9.8	434	10	US-09-430-221-4	Sequence 4, Appl1
25	6	9.8	448	9	US-10-084-994-10	Sequence 10, Appl1
26	6	9.8	464	9	US-10-002-050-20	Sequence 20, Appl
27	6	9.8	464	9	US-10-002-304-20	Sequence 20, Appl
28	6	9.8	464	12	US-10-003-152-20	Sequence 20, Appl
29	6	9.8	469	10	US-09-815-242-11533	Sequence 11533, A
30	6	9.8	510	9	US-09-738-626-6798	Sequence 6798, Ap
31	6	9.8	537	9	US-09-738-626-4471	Sequence 4471, Ap
32	6	9.8	719	9	US-10-007-270-4	Sequence 4, Appl1
33	6	9.8	724	9	US-10-028-072-60	Sequence 60, Appl
34	6	9.8	724	9	US-10-121-049-60	Sequence 60, Appl
35	6	9.8	724	9	US-10-123-904-60	Sequence 60, Appl
36	6	9.8	724	9	US-10-140-470-60	Sequence 60, Appl
37	6	9.8	724	9	US-10-175-746-60	Sequence 60, Appl
38	6	9.8	724	9	US-10-176-921-60	Sequence 60, Appl
39	6	9.8	724	9	US-10-176-921-60	Sequence 60, Appl
40	6	9.8	724	9	US-10-137-865-60	Sequence 60, Appl
41	6	9.8	724	9	US-10-140-474-60	Sequence 60, Appl
42	6	9.8	724	9	US-10-142-431-60	Sequence 60, Appl
43	6	9.8	724	9	US-10-143-114-60	Sequence 60, Appl
44	6	9.8	724	9	US-10-140-002-60	Sequence 60, Appl
45	6	9.8	724	9	US-10-142-419-60	Sequence 60, Appl

## ALIGNMENTS

RESULT 1  
US-09-906-393A-36  
; Sequence 36, Application US/09906393A  
; Publication No. US20030039970A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906,393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-906-393A-36

Query Match 100.0%; Score 61; DB 9; Length 417;  
Best Local Similarity 100.0%; Pred. No. 4.2e-58;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFENYKGNVLINKDRCKDDETHLTLLVPRDNTYEKIDNSQVSSGL 60  
DB 137 CGPGTKKVVHVFENYKGNVLINKDRCKDDETHLTLLVPRDNTYEKIDNSQVSSGL 196

QY 61 E 61  
DB 197 E 197

RESULT 2  
US-09-906-393A-6  
; Sequence 6, Application US/09906393A  
; Publication No. US20030039970A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED

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; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-906-393A-6

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Query Match          19.7%; Score 12; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 21 INKDIRCKDEF 32
Db 1 INKDIRCKDEF 12

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RESULT 3
US-10-078-770-128
; Sequence 128, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 128
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (92)..(93)
; NAME/KEY: UNSURE
; LOCATION: (98)
; NAME/KEY: UNSURE
; LOCATION: (100)
US-10-078-770-128

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Query Match          9.8%; Score 6; DB 9; Length 116;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 16 GKNVLI 21
Db 26 GKNVLI 31

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RESULT 4
US-10-078-770-132
; Sequence 132, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 132
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
US-10-078-770-132

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```

Query Match          9.8%; Score 6; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 16 GKNVLI 21
Db 33 GKNVLI 38

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```

RESULT 5
US-09-925-664-14
; Sequence 14, Application US/09925664
; Patent No. US2002016006A1
; GENERAL INFORMATION:
; APPLICANT: Denney, Jr., Dan W.
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
; FILE REFERENCE: GENTROP-06499
; CURRENT APPLICATION NUMBER: US/09/925,664
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/370,453
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 08/644,664
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/761,277
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-664-14

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Query Match          9.8%; Score 6; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      16 GKNVLI 21
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Db      127 GKNVLI 132

RESULT 6
US-09-189-833B-7
; Sequence 7, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-7

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

OY      16 GKNVLI 21
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Db      127 GKNVLI 132

RESULT 7
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

OY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 8
US-09-902-705-7
; Sequence 7, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-7

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

OY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 9
US-09-902-705-8
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

OY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 10
US-09-895-913A-362
; Sequence 362, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
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; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 226
; TYPE: prt
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 224
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-913A-362
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Query Match          9.8%; Score 6; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      16 GKNVLI 21
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Db       5 GKNVLI 10
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RESULT 11
US-09-815-242-11342
; Sequence 11342, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11342
; LENGTH: 247
; TYPE: prt
; ORGANISM: Helicobacter pylori
US-09-815-242-11342
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Query Match          9.8%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      16 GKNVLI 21
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Db       5 GKNVLI 10
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RESULT 12

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US-09-815-242-11514
; Sequence 11514, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11514
; LENGTH: 247
; TYPE: prt
; ORGANISM: Helicobacter pylori
US-09-815-242-11514
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Query Match          9.8%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      16 GKNVLI 21
        |||||
Db       5 GKNVLI 10
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RESULT 13
US-10-062-254-90
; Sequence 90, Application US/10062254
; Patent No. US2002013882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morganite, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zhu, Qun
; APPLICANT: Zheng, Peizhong
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
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: PRIOR FILING DATE: 2000-07-28
: PRIOR APPLICATION NUMBER: 60/146511
: PRIOR FILING DATE: 1999-07-30
: PRIOR APPLICATION NUMBER: 60/156006
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/156899
: PRIOR FILING DATE: 1999-09-30
: PRIOR APPLICATION NUMBER: 60/157287
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/169767
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 60/171054
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: 60/172958
: PRIOR FILING DATE: 1999-12-21
: PRIOR APPLICATION NUMBER: 60/171515
: PRIOR FILING DATE: 1999-12-22
: PRIOR APPLICATION NUMBER: 60/173535
: PRIOR FILING DATE: 1999-12-29
: NUMBER OF SEQ ID NOS: 375
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 90
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Zea mays
US-10-062-254-90

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Query Match          9.8%; Score 6; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 54 QVESGS 59
Db 28 QVESGS 33

```

```

RESULT 14
US-09-815-242-14056
: Sequence 14056, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14056
: LENGTH: 269
: TYPE: PRT

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: ORGANISM: Salmonella typhi
US-09-815-242-14056

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Query Match          9.8%; Score 6; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 19 VLINKD 24
Db 3 VLINKD 8

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```

RESULT 15
US-09-815-242-11836
: Sequence 11836, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11836
: LENGTH: 295
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11836

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Query Match          9.8%; Score 6; DB 10; Length 285;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 19 VLINKD 24
Db 3 VLINKD 8

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GenCore version 5.1.4-p5.4578  
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Run on: March 14, 2003, 20:41:23 ; Search time 3.38109 Seconds  
(without alignments)  
522.132 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60  
Sequence: 1 GPGTKKVVHVFNYKGNVLI.....PDNTYEYKIDNSQVSGSLE 60

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	11.7	593	1 US-08-296-362-2	Sequence 2, Appl1
2	7	11.7	1009	4 US-09-693-146-4	Sequence 4, Appl1
3	6	10.0	69	4 US-09-134-001C-5362	Sequence 5362, Ap
4	6	10.0	74	4 US-09-134-001C-4815	Sequence 4815, Ap
5	6	10.0	94	4 US-09-134-001C-5410	Sequence 5410, Ap
6	6	10.0	184	3 US-08-630-172-2	Sequence 2, Appl1
7	6	10.0	184	4 US-09-375-419-2	Sequence 2, Appl1
8	6	10.0	185	4 US-09-384-162-11	Sequence 11, Appl1
9	6	10.0	218	1 US-08-644-664B-14	Sequence 14, Appl1
10	6	10.0	218	2 US-08-761-277A-14	Sequence 14, Appl1
11	6	10.0	318	1 US-08-530-950-2	Sequence 2, Appl1
12	6	10.0	318	1 US-08-446-083-2	Sequence 2, Appl1
13	6	10.0	318	4 US-08-888-429A-2	Sequence 2, Appl1
14	6	10.0	318	4 US-09-149-879-2	Sequence 2, Appl1
15	6	10.0	351	4 US-08-466-465-6	Sequence 6, Appl1
16	6	10.0	418	3 US-08-630-172-18	Sequence 18, Appl1
17	6	10.0	418	4 US-09-375-419-18	Sequence 18, Appl1
18	6	10.0	504	4 US-09-499-302A-6	Sequence 6, Appl1
19	6	10.0	512	2 US-08-557-122A-33	Sequence 33, Appl1
20	6	10.0	512	4 US-09-262-666-33	Sequence 33, Appl1
21	6	10.0	812	1 US-08-446-794A-4	Sequence 4, Appl1
22	6	10.0	891	4 US-09-134-001C-4913	Sequence 4913, Ap
23	5	8.3	6	4 US-08-874-197-3	Sequence 3, Appl1
24	5	8.3	6	4 US-08-874-197-7	Sequence 7, Appl1
25	5	8.3	6	4 US-08-648-182-3	Sequence 7, Appl1
26	5	8.3	6	4 US-08-648-182-7	Sequence 7, Appl1
27	5	8.3	10	1 US-08-594-447-12	Sequence 12, Appl1

28	5	8.3	10	1 US-08-541-964-11	Sequence 11, Appl1
29	5	8.3	10	2 US-08-665-647-26	Sequence 26, Appl1
30	5	8.3	12	1 US-08-446-856A-10	Sequence 10, Appl1
31	5	8.3	12	1 US-08-446-856A-11	Sequence 11, Appl1
32	5	8.3	15	1 US-08-447-411-64	Sequence 64, Appl1
33	5	8.3	15	2 US-08-662-227-21	Sequence 21, Appl1
34	5	8.3	15	2 US-08-662-227-22	Sequence 22, Appl1
35	5	8.3	15	4 US-09-017-947-21	Sequence 21, Appl1
36	5	8.3	15	4 US-09-017-947-22	Sequence 22, Appl1
37	5	8.3	20	3 US-08-467-023-38	Sequence 38, Appl1
38	5	8.3	20	3 US-08-467-023-39	Sequence 39, Appl1
39	5	8.3	22	3 US-09-024-020B-18	Sequence 18, Appl1
40	5	8.3	22	4 US-09-425-043-18	Sequence 18, Appl1
41	5	8.3	31	1 US-08-248-021A-4	Sequence 4, Appl1
42	5	8.3	32	1 US-08-248-021A-6	Sequence 6, Appl1
43	5	8.3	36	1 US-08-190-802A-133	Sequence 133, App
44	5	8.3	36	1 US-08-190-802A-177	Sequence 177, App
45	5	8.3	36	4 US-08-477-346-133	Sequence 133, App

## ALIGNMENTS

RESULT 1  
US-08-296-362-2  
; Sequence 2, Application US/08296362  
; Patent No. 5691306  
; GENERAL INFORMATION:  
; APPLICANT: Bergeron, John J.M.  
; APPLICANT: Thomas, David Y.  
; APPLICANT: Wada, Ikuo  
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF  
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/296,362  
; FILING DATE: 25-AUG-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deehr, Manya S.  
; REGISTRATION NUMBER: 37,120  
; REFERENCE/DOCKET NUMBER: 690066.401C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELE: 3723836  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 593 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein.  
; US-08-296-362-2  
Query Match 11.7%; Score 7; DB 1; Length 593;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 THLYPLI 38  
|||||||

DB 236 THLYTLI 242

RESULT 2  
US-09-693-146-4

; Sequence 4, Application US/09693146  
; Patent No. 6413758  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Shuang-yong  
; APPLICANT: Zhu, Zhenyu  
; APPLICANT: Xiao, Jian-ping  
; TITLE OF INVENTION: Method For Cloning And Expression Of Bpm1 Restriction  
; TITLE OF INVENTION: Endonuclease In E. coli  
; FILE REFERENCE: NEB-183  
; CURRENT APPLICATION NUMBER: US/09/693,146  
; CURRENT FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1009  
; TYPE: PRT  
; ORGANISM: Bacillus pumilus  
US-09-693-146-4

Query Match 11.7%; Score 7; DB 4; Length 1009;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFNYKKG 16  
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DB 741 IFNYKKG 747RESULT 3  
US-09-134-001C-5362

; Sequence 5362, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NOCLETIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5362  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5362

Query Match 10.0%; Score 6; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22  
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DB 29 NVLINK 34RESULT 4  
US-09-134-001C-4815

; Sequence 4815, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NOCLETIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4815  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4815

Query Match 10.0%; Score 6; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTLI 38  
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DB 15 HLYTLI 20RESULT 5  
US-09-134-001C-5410

; Sequence 5410, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NOCLETIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5410  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5410

Query Match 10.0%; Score 6; DB 4; Length 94;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22  
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DB 21 NVLINK 26RESULT 6  
US-08-630-172-2

; Sequence 2, Application US/08630172  
; Patent No. 6060054  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-2

Query Match 10.0%; Score 6; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 KGKNVL 19  
|||||  
DB 89 KGKNVL 94

RESULT 7  
US-09-375-419-2  
Sequence 2, Application US/09375419  
Patent No. 6264950

GENERAL INFORMATION:  
APPLICANT: Staerz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
TITLE OF INVENTION: LYMPHOCYTE VETO  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/375,419  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,172  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-375-419-2

Query Match 10.0%; Score 6; DB 4; Length 184;

Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 KGKNVL 19  
|||||  
DB 89 KGKNVL 94

RESULT 8  
US-09-384-162-11  
Sequence 11, Application US/09384162  
Patent No. 6376747

GENERAL INFORMATION:  
APPLICANT: xing, Ti  
APPLICANT: Malik, Kamal  
APPLICANT: Martin-Heller, Teresa  
APPLICANT: Miki L., Brian  
TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase  
FILE REFERENCE: 08-884280US  
CURRENT APPLICATION NUMBER: US/09/384,162  
CURRENT FILING DATE: 1999-08-27  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 11  
LENGTH: 185  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-384-162-11

Query Match 10.0%; Score 6; DB 4; Length 185;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22  
|||||  
DB 108 NVLINK 113

RESULT 9  
US-08-644-664B-14  
Sequence 14, Application US/08644664B  
Patent No. 5776746

GENERAL INFORMATION:  
APPLICANT: Denney, Jr., Dan W.  
TITLE OF INVENTION: Gene Amplification Methods  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/644,664B  
FILING DATE: 01-MAY-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: GENIOTPE-00912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-644-664B-14

Query Match 10.0%; Score 6; DB 1; Length 218;  
Best local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20  
DB 127 GKNVLI 132

## RESULT 10

US-08-761-277A-14  
Sequence 14, Application US/08761277A  
Patent No. 5972334  
GENERAL INFORMATION:  
APPLICANT: Denney Jr., Dan W.  
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,277A  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/644,664  
FILING DATE: 01-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: GENITOPE-02406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ. ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-761-277A-14

Query Match 10.0%; Score 6; DB 2; Length 218;  
Best local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20  
DB 127 GKNVLI 132

## RESULT 11

US-08-530-950-2  
Sequence 2, Application US/08530950  
Patent No. 5736381  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Raingeaud, Joel  
APPLICANT: Gupta, Shashi

APPLICANT: Defiard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/530,950  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
US-08-530-950-2

Query Match 10.0%; Score 6; DB 1; Length 318;  
Best local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22  
DB 166 NVLINK 171

## RESULT 12

US-08-446-083-2.  
Sequence 2, Application US/08446083  
Patent No. 5804427  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Raingeaud, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Defiard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,083

FILING DATE: 19-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 04020/066001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-446-083-2

Query Match 10.0%; Score 6; DB 1; Length 318;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22  
166 NVLINK 171

Db 166 NVLINK 171

RESULT 13  
US-08-888-429A-2  
; Sequence 2, Application US/08888429A  
; Patent No. 6136596  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Whitmarsh, Alan  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTED for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, Peter J.  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 299354  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

FRAGMENT TYPE: internal  
US-08-888-429A-2

Query Match 10.0%; Score 6; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22  
166 NVLINK 171

Db 166 NVLINK 171

RESULT 14  
US-09-149-879-2  
; Sequence 2, Application US/09149879  
; Patent No. 6174676  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Raingeaud, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Derjard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/149,879  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
US-09-149-879-2

Query Match 10.0%; Score 6; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22  
166 NVLINK 171

Db 166 NVLINK 171

RESULT 15  
US-08-466-465-6  
; Sequence 6, Application US/08466465  
; Patent No. 6162432

GENERAL INFORMATION:  
APPLICANT: Wallner, Barbara P.  
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen  
TITLE OF INVENTION: Method of Presenting Cell Driven Skin Conditions Using  
TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,465  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/08755  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/862,022  
FILING DATE: 12-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/770,969  
FILING DATE: 07-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis (PLM)  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: BGP-111CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-466-465-6

Query Match 10.0%; Score 6; DB 4; Length 351;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 KGNVYL 19  
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DB 113 KGNVYL 118

Search completed: March 14, 2003, 20:50:10  
Job time : 4.38109 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 2.92264 Seconds

(without alignments)  
946.243 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60

Sequence: 1 GPGRKKVHVIFNYKGNKLVIL.....PDNTYEKIDNSQVESGSL 60

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/2/pubppa/PCN\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB pep:\*
- 6: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB pep:\*
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- 8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB pep:\*
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- 13: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB pep:\*
- 14: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	417	9	US-09-906-393A-36
2	12	20.0	12	9	US-09-906-393A-6
3	6	10.0	116	9	US-10-078-770-128
4	6	10.0	125	9	US-10-078-770-132
5	6	10.0	218	9	US-09-925-664-14
6	6	10.0	218	10	US-09-189-833B-7
7	6	10.0	218	10	US-09-189-833B-8
8	6	10.0	218	10	US-09-302-705-7
9	6	10.0	218	10	US-09-902-705-8
10	6	10.0	226	9	US-09-895-913A-362
11	6	10.0	247	10	US-09-815-242-11342
12	6	10.0	247	10	US-09-815-242-11514
13	6	10.0	250	12	US-10-062-254-90
14	6	10.0	289	10	US-09-815-242-14056
15	6	10.0	295	10	US-09-966-459A-10
16	6	10.0	312	9	US-09-966-459A-10
17	6	10.0	318	10	US-09-761-569-2
18	6	10.0	351	10	US-09-796-033-6
19	6	10.0	351	10	US-09-730-465-6

20	6	10.0	411	9	US-10-002-050-10	Sequence 10, Appl
21	6	10.0	411	9	US-10-002-304-10	Sequence 10, Appl
22	6	10.0	411	12	US-10-003-152-10	Sequence 10, Appl
23	6	10.0	423	10	US-09-729-674-160	Sequence 160, Appl
24	6	10.0	434	10	US-09-430-221-4	Sequence 4, Appl
25	6	10.0	464	9	US-10-002-050-20	Sequence 20, Appl
26	6	10.0	464	9	US-10-002-304-20	Sequence 20, Appl
27	6	10.0	464	12	US-10-003-152-20	Sequence 20, Appl
28	6	10.0	469	10	US-09-815-242-11533	Sequence 11533, A
29	6	10.0	510	9	US-09-738-626-6798	Sequence 6798, Ap
30	6	10.0	537	9	US-09-738-626-4471	Sequence 4471, Ap
31	6	10.0	724	9	US-10-028-072-60	Sequence 60, Appl
32	6	10.0	724	9	US-10-121-049-60	Sequence 60, Appl
33	6	10.0	724	9	US-10-123-904-60	Sequence 60, Appl
34	6	10.0	724	9	US-10-140-474-60	Sequence 60, Appl
35	6	10.0	724	9	US-10-140-474-60	Sequence 60, Appl
36	6	10.0	724	9	US-10-175-746-60	Sequence 60, Appl
37	6	10.0	724	9	US-10-176-918-60	Sequence 60, Appl
38	6	10.0	724	9	US-10-137-865-60	Sequence 60, Appl
39	6	10.0	724	9	US-10-140-474-60	Sequence 60, Appl
40	6	10.0	724	9	US-10-142-431-60	Sequence 60, Appl
41	6	10.0	724	9	US-10-143-114-60	Sequence 60, Appl
42	6	10.0	724	9	US-10-140-002-60	Sequence 60, Appl
43	6	10.0	724	9	US-10-142-419-60	Sequence 60, Appl
44	6	10.0	840	9	US-10-078-770-134	Sequence 134, App
45	6	10.0	948	9	US-09-738-626-6040	Sequence 6040, Ap

## ALIGNMENTS

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RESULT 1
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906, 393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218, 761
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match      100.0%; Score 60; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 86-57;
Matches 60; Conservative 0; Mismatches 0; Indels 0;

QY      1  GPGRKKVHVIFNYKGNKLVILNKDICKDDEFTHTLTLIVRPNMTYEKIDNSQVESGSL 60
Db      138 GPGRKKVHVIFNYKGNKLVILNKDICKDDEFTHTLTLIVRPNMTYEKIDNSQVESGSL 197

RESULT 2
US-09-906-393A-6
; Sequence 6, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906, 393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218, 761
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;; PRIOR FILING DATE: 2000-07-17  
;; NUMBER OF SEQ ID NOS: 36  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO: 6  
;; LENGTH: 12  
;; TYPE: PRF  
;; ORGANISM: homo sapiens  
US-09-906-393A-6

Query Match 20.0%; Score 12; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 INKDIRCKDEF 31  
DB 1 INKDIRCKDEF 12

RESULT 3  
US-10-078-770-128  
;; Sequence 128, Application US/10078770  
;; Publication No. US20030003471A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Famodu, Omolayo O.  
;; APPLICANT: Miao, Guo-Hua  
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides  
;; FILE REFERENCE: BB-1365 US NA  
;; CURRENT APPLICATION NUMBER: US/10/078,770  
;; PRIOR FILING DATE: 2002-02-19  
;; PRIOR APPLICATION NUMBER: 09/614,188  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,400  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/153,534  
;; PRIOR FILING DATE: 1999-08-13  
;; PRIOR APPLICATION NUMBER: 60/161,223  
;; PRIOR FILING DATE: 1999-10-22  
;; PRIOR APPLICATION NUMBER: 60/159,878  
;; PRIOR FILING DATE: 1999-10-15  
;; PRIOR APPLICATION NUMBER: 60/157,401  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/143,419  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,409  
;; PRIOR FILING DATE: 1999-07-12  
;; NUMBER OF SEQ ID NOS: 196  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO: 128  
;; LENGTH: 116  
;; TYPE: PRF  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: UNSURE  
;; LOCATION: (92)-(93)  
;; NAME/KEY: UNSURE  
;; LOCATION: (98)  
;; NAME/KEY: UNSURE  
;; LOCATION: (100)  
US-10-078-770-128

Query Match 10.0%; Score 6; DB 9; Length 116;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20  
DB 26 GKNVLI 31

RESULT 4  
US-10-078-770-132  
;; Sequence 132, Application US/10078770

;; Publication No. US20030003471A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Famodu, Omolayo O.  
;; APPLICANT: Forge, Charlie  
;; APPLICANT: Miao, Guo-Hua  
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides  
;; FILE REFERENCE: BB-1365 US NA  
;; CURRENT APPLICATION NUMBER: US/10/078,770  
;; PRIOR FILING DATE: 2002-02-19  
;; PRIOR APPLICATION NUMBER: 09/614,188  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,400  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/153,534  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: 60/161,223  
;; PRIOR FILING DATE: 1999-10-22  
;; PRIOR APPLICATION NUMBER: 60/159,878  
;; PRIOR FILING DATE: 1999-10-15  
;; PRIOR APPLICATION NUMBER: 60/157,401  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/143,419  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,409  
;; PRIOR FILING DATE: 1999-07-12  
;; NUMBER OF SEQ ID NOS: 196  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO: 132  
;; LENGTH: 125  
;; TYPE: PRF  
;; ORGANISM: Zea mays  
US-10-078-770-132

Query Match 10.0%; Score 6; DB 9; Length 125;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20  
DB 33 GKNVLI 38

RESULT 5  
US-09-925-664-14  
;; Sequence 14, Application US/09925664  
;; Patent No. US2002016006A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Denney, Jr., Dan W.  
;; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia  
;; FILE REFERENCE: GENTOPE-06499  
;; CURRENT APPLICATION NUMBER: US/09/925,664  
;; PRIOR FILING DATE: 2001-08-09  
;; PRIOR APPLICATION NUMBER: 09/370,453  
;; PRIOR FILING DATE: 1999-08-09  
;; PRIOR APPLICATION NUMBER: 08/644,664  
;; PRIOR FILING DATE: 1996-05-01  
;; PRIOR APPLICATION NUMBER: 08/761,277  
;; PRIOR FILING DATE: 1996-12-06  
;; NUMBER OF SEQ ID NOS: 80  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO: 14  
;; LENGTH: 218  
;; TYPE: PRF  
;; ORGANISM: Mus musculus  
US-09-925-664-14

Query Match 10.0%; Score 6; DB 9; Length 218;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20  
DB 127 GKNVLI 132



```
RESULT 6
US-09-189-833B-7
; Sequence 7, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-7

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
|||||
Db 127 GKNVLI 132

RESULT 7
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
|||||
Db 127 GKNVLI 132

RESULT 8
US-09-902-705-7
; Sequence 7, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
```

```
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-7

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
|||||
Db 127 GKNVLI 132

RESULT 9
US-09-902-705-8
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
|||||
Db 127 GKNVLI 132

RESULT 10
US-09-895-913A-362
; Sequence 362, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/81,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 362
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 224
; OTHER INFORMATION: Xaa - Any Amino Acid
US-09-895-913A-362
```

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Query Match          10.0%; Score 6; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 15 GKNVLI 20
    |||||
DB 5 GKNVLI 10
```

RESULT 11

```
US-09-815-242-11342
; Sequence 11342, Application US/09815242
; Patent No. US20020061569A1
```

GENERAL INFORMATION:

```
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
```

```
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
```

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11342

LENGTH: 247

TYPE: PRT

ORGANISM: Helicobacter pylori

US-09-815-242-11342

```
Query Match          10.0%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 15 GKNVLI 20
    |||||
DB 5 GKNVLI 10
```

RESULT 12

US-09-815-242-11514

Sequence 11514, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

```
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
```

```
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
```

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11514

LENGTH: 247

TYPE: PRT

ORGANISM: Helicobacter pylori

US-09-815-242-11514

```
Query Match          10.0%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 15 GKNVLI 20
    |||||
DB 5 GKNVLI 10
```

RESULT 13

US-10-062-254-90

Sequence 90, Application US/10062254

Patent No. US2002013882A1

GENERAL INFORMATION:

```
APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Fang, Yiwen
APPLICANT: Hantke, Sabine S.
APPLICANT: Lee, Jian-Ming
APPLICANT: Li, Zhongsen
APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Niu, Xiping
APPLICANT: Odell, Joan
```

APPLICANT: Rafalski, Antoni

APPLICANT: Sakai, Hajime

APPLICANT: Zheng, Peizhong

APPLICANT: Zhu, Qun

TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/062,254

PRIOR FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 09/630,346

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: 60/146511

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 60/156006

```

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 90
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Zea mays
US-10-062-254-90

Query Match      10.0%; Score 6; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 QVSGS 58
Db 28 QVSGS 33

RESULT 14
US-09-815-242-14056
; Sequence 14056, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14056
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-14056

Query Match      10.0%; Score 6; DB 10; Length 289;
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```

Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 VLINRD 23
Db 3 VLINRD 8

RESULT 15
US-09-815-242-11836
; Sequence 11836, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11836
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11836

Query Match      10.0%; Score 6; DB 10; Length 295;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 VLINRD 23
Db 3 VLINRD 8

Search completed: March 14, 2003, 20:51:12
Job time : 3.92264 secs
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GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 8.02292 Seconds  
(without alignments)  
1540.938 Million cell updates/sec

Title: US-09-807-148-8  
Perfect score: 60  
Sequence: 1 GPGTKKHVHVFYFKGNVLI.....PDNTYEYKINDSQVESGSL 60

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

SPREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	41	68.3	417	6	Q8SQ53 bos taurus
2	22	36.7	343	13	Q91711 xenopus lae
3	22	36.7	411	13	Q91710 xenopus lae
4	20	33.3	419	13	Q98984 rana rugosa
5	19	31.7	405	5	Q26268 aplysia cal
6	18	30.0	421	5	Q9U650 strongyloce
7	17	28.3	318	13	Q9PTX7 letheion
8	17	28.3	410	5	Q16893 amblyomma a
9	14	23.3	214	4	Q9UDG2 homo sapien
10	13	21.7	395	5	Q96722 taenia soli
11	13	21.7	406	5	Q9U916 drosophila
12	12	20.0	350	5	Q26514 schistosoma
13	12	20.0	396	5	Q45034 schistosoma
14	12	20.0	417	13	Q9PUC1 brachydanio
15	12	20.0	559	5	Q9NG26 tritrichomo
16	11	18.3	375	5	Q18478 lltomosoido

17	11	18.3	387	5	Q97372	097372 dicrofilaria
18	11	18.3	397	5	Q8WPG8	Q8WPG8 gallieria me
19	11	18.3	406	5	Q8WR36	Q8WR36 anopheles g
20	11	18.3	407	5	Q8T903	Q8T903 aedes aegypt
21	10	16.7	415	5	Q8WRU9	Q8WRU9 meloidogyne
22	9	15.0	403	5	Q76961	Q76961 necator ame
23	8	13.3	137	11	Q9D373	Q9D373 mus musculus
24	8	13.3	380	11	Q9D906	Q9D906 mus musculus
25	8	13.3	384	4	Q96LN3	Q96LN3 homo sapien
26	8	13.3	384	4	Q96L12	Q96L12 homo sapien
27	7	11.7	141	5	Q8THJ8	Q8THJ8 methanosarc
28	7	11.7	215	6	Q8SR0	Q8SR0 dictyostel
29	7	11.7	231	5	Q9TSM7	Q9TSM7 canis sp. b
30	7	11.7	231	5	Q96085	Q96085 plasmodium
31	7	11.7	279	17	Q8U458	Q8U458 pyrococcus
32	7	11.7	280	1	Q52958	Q52958 pyrococcus
33	7	11.7	321	13	Q9U5G0	Q9U5G0 eptaretus
34	7	11.7	358	9	Q64099	Q64099 bacterioph
35	7	11.7	358	16	Q34336	Q34336 bacillus su
36	7	11.7	397	17	Q8U0M5	Q8U0M5 pyrococcus
37	7	11.7	511	16	Q8XXY7	Q8XXY7 ralstonia s
38	7	11.7	519	5	Q8SR76	Q8SR76 encaphalito
39	7	11.7	801	10	Q942X7	Q942X7 oryza sativ
40	7	11.7	910	10	Q8VMY9	Q8VMY9 pinus pinas
41	7	11.7	1373	4	Q9Y2E5	Q9Y2E5 homo sapien
42	7	11.7	1461	10	Q9S1M3	Q9S1M3 arabidopsis
43	6	10.0	76	6	Q97871	Q97871 isoodon mac
44	6	10.0	76	6	Q97872	Q97872 isoodon mac
45	6	10.0	76	6	Q97873	Q97873 macropus eu

## ALIGNMENTS

## RESULT 1

ID Q8SQ53 PRELIMINARY: PRT: 417 AA.  
AC Q8SQ53.  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Calreticulin.  
GN CRT.  
OS Bos taurus (bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hossain M.A., Takuwa K., Minakata H., Nakajima T.,  
RT "Bovine brain calreticulin."  
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AB067687; BAB86913.1; -  
SQ SEQUENCE 417 AA: 48038 MW: 79F812C75417B95 CXC64;

Query Match 68.3%; Score 41; DB 6; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.4e-36;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVHVFYFKGNVLIINDICKRDEFTHTLTVLRP 41  
DB 138 GPGTKKHVHVFYFKGNVLIINDICKRDEFTHTLTVLRP 178

## RESULT 2

ID Q91711 PRELIMINARY: PRT: 343 AA.  
AC Q91711.  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin (Fragment).

```
05 Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS.
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS.";
RL Biochem. J. 0:0-0(0).
DR EMBL: X67598; CAA47867.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN.REPEAT.3.
FT NON_TER 1
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match
Best Local Similarity 36.7%; Score 22; DB 13; Length 343;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 FTHLYTLIVRPDNTYEKIDNS 52
DB 140 FTHLYTLIVRPDNTYEKIDNS 161
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ID 091710 PRELIMINARY; PRT; 411 AA.
AC 091710;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS.
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS.";
RL Biochem. J. 0:0-0(0).
DR EMBL: X67597; CAA47866.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN.REPEAT.2.
FT SIGNAL 1
FT NON_TER 1
FT SIGNAL <1 12 POTENTIAL.
FT CHAIN 13 411 CALRETICULIN.
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E0DEBEFA CRC64;

Query Match
Best Local Similarity 36.7%; Score 22; DB 13; Length 411;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 FTHLYTLIVRPDNTYEKIDNS 52
DB 163 FTHLYTLIVRPDNTYEKIDNS 184
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```

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RESULT 4
OY 098984 PRELIMINARY; PRT; 419 AA.
AC 098984;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Calreticulin.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of the
RT frog, Rana rugosa.";
RT J. Exp. Zool. 275:431-443(1996).
RL EMBL: D78589; BAA11425.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN.REPEAT.3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match
Best Local Similarity 33.3%; Score 20; DB 13; Length 419;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLIVRPDNTYEKIDNS 52
DB 171 HLYTLIVRPDNTYEKIDNS 190
|||||
ID 026268 PRELIMINARY; PRT; 405 AA.
AC 026268;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Calreticulin.
GN CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiidae;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL: S51239; AAB24569.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
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DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; CALRETICULIN.1.  
DR PROSITE; PS00803; CALRETICULIN.1.1.  
DR PROSITE; PS00804; CALRETICULIN.2.1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN.1.  
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 31.7%; Score 19; DB 5; Length 405;  
Best Local Similarity 100.0%; Pred. No. 1.7e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTLIVRPDNTYEKIDN 51  
|||||  
Db 166 HLYTLIVRPDNTYEKIDN 184

RESULT 6  
Q0U6S0 PRELIMINARY; PRT; 421 AA.  
AC Q0U6S0;  
DT 01-MAY-2000 (TREMBlrel.13, Created)  
DT 01-MAY-2000 (TREMBlrel.13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel.17, Last annotation update)  
DE Calreticulin precursor.  
GN CALRET.  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidae; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Susan J.M., Just M.L., Lennarz W.J.;  
RT Cloning and Characterization of Alphan Integrin and Calreticulin in  
RT Embryos of the Sea Urchin."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF17915; AAD5725.1; "  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER\_target.  
DR Pfam; PF00262; calreticulin.1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; CALRETICULIN.1.  
DR PROSITE; PS00804; CALRETICULIN.2.1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN.1.  
KM Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 421 CALRETICULIN.  
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 30.0%; Score 18; DB 5; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.1e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KDIRCKDEFTHTLV 39  
|||||  
Db 158 KDIRCKDEFTHTLV 175

RESULT 7  
Q9PTX7 PRELIMINARY; PRT; 318 AA.  
AC Q9PTX7;  
DT 01-MAY-2000 (TREMBlrel.13, Created)  
DT 01-MAY-2000 (TREMBlrel.13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel.19, Last annotation update)  
DE Calreticulin (Fragment).  
OS Lethenteron reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lethenteron.  
OX NCBI\_TaxID=7753;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20063780; PubMed=10594174;  
RA Kuraku S., Hoshiyama D., Katch K., Suga H., Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
RT genes."  
RL J. Mol. Evol. 49:729-735(1999).  
DR EMBL; AB025328; BAA8481.1; "  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER\_target.  
DR Pfam; PF00262; calreticulin.1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin.1.  
DR PROSITE; PS00804; CALRETICULIN.2.1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN.1.  
FT NON\_TER 1 1  
SQ SEQUENCE 318 AA; 36997 MW; C88102EAC1506 CRC64;

Query Match 28.3%; Score 17; DB 13; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHIFNYKGN 17  
|||||  
Db 37 GPGTKKVVHIFNYKGN 53

RESULT 8  
Q16893 PRELIMINARY; PRT; 410 AA.  
AC Q16893;  
DT 01-NOV-1996 (TREMBlrel.01, Created)  
DT 01-JAN-1999 (TREMBlrel.09, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel.17, Last annotation update)  
DE Calreticulin.  
GN CRT-1.  
OS Amblyomma americanum.  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
OX NCBI\_TaxID=6943;  
RN [1]  
RP SEQUENCE OF 49-410 FROM N.A.  
RA TISSUE-SALIVARY GLANDS;  
RC Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,  
RA Needham G.R.;  
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
RT saliva."  
RT J. Insect Physiol. 41:369-375(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLANDS;  
RA Jaworski D.C.;  
RN Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLANDS;  
RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U07708; AAC79094.1; "  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER\_target.  
DR Pfam; PF00262; calreticulin.1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin.1.  
DR PROSITE; PS00803; CALRETICULIN.1.1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT.3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN.1.  
SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 28.3%; Score 17; DB 5; Length 410;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFNYKGN 17  
 |||  
 DB 137 GPGTKKVVHVFNYKGN 153

## RESULT 9

Q9UDG2 PRELIMINARY: PRT; 214 AA.

AC Q9UDG2: 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-JUN-2000 (TREMBLrel. 21, Last annotation update)  
 DE CALRETICULIN-CALCIUM binding protein (Fragments).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95143082; PubMed=7841019;  
 RA Houten G., Koch C.;  
 RT "Human placental calreticulin: purification, characterization and  
 association with other proteins."  
 RT Acta Chem. Scand 48:905-911(1994).  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF001866; Calreticulin; 1.  
 FT NON\_TER 1 1  
 FT NON\_CONS 31 32  
 FT NON\_CONS 59 60  
 FT NON\_CONS 78 79  
 FT NON\_CONS 116 117  
 FT NON\_TER 214 214  
 SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;  
 Query Match 23.3%; Score 14; DB 4; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 2,8e-07;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 VKINDSVEGSGSLE 60  
 |||  
 DB 95 VKINDSVEGSGSLE 108

## RESULT 10

Q96722 PRELIMINARY: PRT; 395 AA.

AC Q96722: 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Calcium binding protein calreticulin precursor.  
 OS Taenia solium.  
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
 OC Cyclophyllidae; Taeniidae; Taenia.  
 OX NCBI\_TaxID=6204;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mendlovic F., Ostoa-Saloma P., Flisser A., Lachette J.P.;  
 RT "Molecular characterization of Taenia solium calreticulin."  
 RT Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 DE EMBL: AF340232; AAK52725.1.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR Pfam: PF001866; calreticulin; 1.  
 DR PRODOM: PD001866; calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_2; UNKNOWN\_1.  
 DR PROSITE: PS00804; CALRETICULIN\_1; UNKNOWN\_1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; UNKNOWN\_1.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW signal.  
 RL Submitted (AUG-1993) to the EMBL/Genbank/DBJ databases.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT SIGNAL 395 AA; 45574 MW; IF317848074335FE CRC64;  
 DR SEQUENCE

Query Match 21.7%; Score 13; DB 5; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 6e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 YTLIVRPDNTYEV 44  
 |||  
 DB 168 YTLIVRPDNTYEV 180

## RESULT 11

Q9U916 PRELIMINARY: PRT; 406 AA.

AC Q9U916: 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN  
 GN CRC OR CG9429.  
 OS Drosophila melanogaster (Fruit Fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OREGON-R;  
 RA Dodo K., Sakoyama Y., Gamo S.;  
 RT "Drosophila melanogaster calreticulin for mRNA."  
 RT Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 DE EMBL: AB000718; BAA85379.1.  
 DR FLYBASE: FBgn0005585; Ctc.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 406 AA; 46809 MW; 6BBA49A6B81CC427 CRC64;  
 Query Match 21.7%; Score 13; DB 5; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 YTLIVRPDNTYEV 47  
 |||  
 DB 172 YTLIVRPDNTYEV 184

## RESULT 12

Q26514 PRELIMINARY: PRT; 350 AA.

AC Q26514: 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin (Fragments).  
 GN RAL-1  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiidae;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CHINESE;  
 RA Huggins M.C., Mooney N.A.;  
 RT "Cloning of a gene encoding a Schistosoma japonicum vaccine candidate  
 with homology to a human Ro/SS-A autoantigen."  
 RT Submitted (AUG-1993) to the EMBL/Genbank/DBJ databases.  
 DE EMBL: M80524; AAB29917.1.  
 DR InterPro: IPR001580; Calreticulin.



DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 350 AA; 40385 MW; 30FBA4EBB685D1C CRC64;  
  
Query Match 20.0%; Score 12; DB 5; Length 350;  
Best Local Similarity 100.0%; Pred. No. 6.7e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 32 THLYTLIVRPDN 43  
Db 122 THLYTLIVRPDN 133  
  
RESULT 13  
Q45034 PRELIMINARY; PRT; 396 AA.  
AC Q45034;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Calreticulin.  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_Taxid=6182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PHILIPPINE.  
RX MEDLINE=21165812; Pubmed=11269324;  
RA Scott J.C., McManus D.P.;  
RT "Molecular cloning and functional expression of a cDNA encoding the  
RT major endoplasmic reticulum-associated calcium-binding protein,  
RT Calreticulin, from Philippine strain Schistosoma japonicum.";  
RL Parasitol. Int. 48:35-46(1999).  
EMBL: AF044408; AAC00515.1; -  
DR EMBL: AF044408; AAC00515.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 396 AA; 45814 MW; C57394C6FB4CD77B CRC64;  
  
Query Match 20.0%; Score 12; DB 5; Length 396;  
Best Local Similarity 100.0%; Pred. No. 7.5e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 32 THLYTLIVRPDN 43  
Db 168 THLYTLIVRPDN 179  
  
RESULT 14  
Q9PUC1 PRELIMINARY; PRT; 417 AA.  
AC Q9PUC1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Calreticulin.  
GN CALR.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_Taxid=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20190113; Pubmed=10660676;  
RA Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.;  
RT "Genes dependent on zebrafish cyclops function identified by AFLP  
RT differential gene expression screen.";  
RL Genes 26:86-97(2000).  
DR EMBL: AF195882; AAF13700.1; -  
DR ZFIN: ZDB-GENE-000208-17; calr.  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 417 AA; 48723 MW; 200C5B400469986 CRC64;  
  
Query Match 20.0%; Score 12; DB 13; Length 417;  
Best Local Similarity 100.0%; Pred. No. 7.8e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 TKRVHVFNNKG 15  
Db 141 TKRVHVFNNKG 152  
  
RESULT 15  
Q9NG26 PRELIMINARY; PRT; 559 AA.  
AC Q9NG26;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Calreticulin-like protein precursor.  
OS Trilichomonas suis.  
OC Eukaryota; Parabasalidae; Trichomonadida; Trichomonadidae;  
OC Trilichomonas.  
OX NCBI\_Taxid=56690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1/N;  
RX MEDLINE=20264030; Pubmed=10802323;  
RA Felleisen R.S.J., Hemphill A., Ingold K., Gottstein B.;  
RT "Conservation of calnexin in the early branching protozoan  
RT Trilichomonas suis.";  
RL Mol. Biochem. Parasitol. 108:109-117(2000).  
EMBL: AJ011990; CAB92410.1; -  
DR EMBL: AJ011990; CAB92410.1; -  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
KW Signal.  
FT SIGNAL 1  
SQ SEQUENCE 559 AA; 63303 MW; 863407D8963EE42D CRC64;  
  
Query Match 20.0%; Score 12; DB 5; Length 559;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 32 THLYTLIVRPDN 43  
Db 186 THLYTLIVRPDN 197

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# OM protein - protein search, using sw model

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(without alignments)  
1085.643 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60  
Sequence: 1 GPGTKKHVIFENYKGNVLI.....PDNTYEYKIDNSQVSGSLE 60

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	416	1 CRTG_MOUSE	P14211 mus musculu
2	60	100.0	416	1 CRTG_MOUSE	P18418 rattus norv
3	60	100.0	417	1 CRTG_HUMAN	P27797 homo sapien
4	60	100.0	418	1 CRTG_HUMAN	P15253 oryctolagus
5	41	68.3	400	1 CRT1_BOVIN	P52193 bos taurus
6	41	68.3	421	1 CRT2_BOVIN	P42918 bos taurus
7	14	23.3	393	1 CRTG_SCHMA	O06814 schistosoma
8	11	18.3	406	1 CRTG_DROME	P11012 drosophila
9	11	18.3	395	1 CRTG_CAEEL	P27798 caenorhadi
10	11	11.7	93	1 HMCI_METBA	P06116 methanosarc
11	7	11.7	93	1 HMCI_METTE	P12770 methanosarc
12	7	11.7	397	1 RPA2_PYRAB	O94113 pyrococcus
13	7	11.7	397	1 RPA2_PYRAB	O84005 pyrococcus
14	7	11.7	397	1 RPA2_PYRAB	O93777 pyrococcus
15	7	11.7	414	1 PCK_SCHPO	O60101 schizosacch
16	7	11.7	591	1 CALX_MOUSE	P35564 mus musculu
17	7	11.7	591	1 CALX_MOUSE	P35565 rattus norv
18	7	11.7	591	1 CALX_MOUSE	P27824 homo sapien
19	7	11.7	591	1 CALX_MOUSE	P27824 homo sapien
20	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
21	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
22	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
23	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
24	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
25	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
26	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
27	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
28	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
29	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
30	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
31	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
32	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
33	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien

## ALIGNMENTS

RESULT 1	ID	CRTG_MOUSE	STANDARD	PRT	416 AA
AC	P14211				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60).				
GN	CALR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid:10090;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.				
RC	STRAIN-BALB/c; TISSUE-Liver;				
RX	MEDLINE=90059955; PubMed=2583110;				
RA	Smith M.J., Koch G.L.E.;				
RT	"Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";				
RL	EMBO J. 8:3581-3586(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93013037; PubMed=1398135;				
RA	Mazzarella R.A., Gold P., Cunningham M., Green M.;				
RT	"Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";				
RL	Gene 120:217-225(1992).				
RN	[3]				
RP	SEQUENCE OF 18-38.				
RC	TISSUE-Fibroblast;				
RX	MEDLINE=9509907; PubMed=7523108;				
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;				
RT	"Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis.";				
RL	Electrophoresis 15:735-745(1994).				
CC	- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.				
CC	- SUBUNIT: MONOMER (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.				
CC	- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.				
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	EMBL; X14926; CA33053.1; -				
DR	EMBL; M92888; AAA37569.1; -				
DR	PIR; S06763; S06763.				
DR	PIR; J01444; J01444.				
DR	SWISS-2DPAGE; P14211; MOUSE.				
DR	MGD; MGI:88252; Calr.				

DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00014; ER\_TARGET; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 416 CALRETICULIN.  
FT DOMAIN 18 197 N-DOMAIN.  
FT DOMAIN 198 308 P-DOMAIN.  
FT DOMAIN 309 416 C-DOMAIN.  
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
FT REPEAT 191 202 1-1.  
FT REPEAT 210 221 1-2.  
FT REPEAT 227 238 1-3.  
FT REPEAT 244 255 1-4.  
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.  
FT REPEAT 269 297 2-1.  
FT REPEAT 273 283 2-2.  
FT REPEAT 287 297 2-3.  
FT REPEAT 351 407 ASP/GLU/LYS-RICH.  
FT DISULFID 137 153 BR SIMILARITY.  
FT SITE 413 416 PREVENT SECRETION FROM ER.  
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D CRC64;

Query Match 100.0%; Score 60; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred No. 1.7e-55;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGTKKVVHIFNKGKGNVLINCKDEFTLTYLIVRPDVTYKIDNSVSGSSGLE 60  
Db 138 GPGTKKVVHIFNKGKGNVLINCKDEFTLTYLIVRPDVTYKIDNSVSGSSGLE 197  
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RESULT 2  
CRTC\_RAT STANDARD; PRT; 416 AA.  
AC P18418; P10452;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Calreticulin precursor (CRP5) (Calregulin) (HACBP) (ERP60) (CALBP)  
DE (Calcium-binding protein 3) (CABP3).  
GN CALR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;  
RX MEDLINE=90370496; PubMed=2395661;  
RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,  
RA Holmes C., Patel Y.C.;  
RT "Structural homology between the rat calreticulin gene product and  
RT the Onchocerca volvulus antigen Ral-1.";  
RL Nucleic Acids Res. 18:4933-4933(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Sprague-Dawley;  
RX MEDLINE=93202172; PubMed=8453984;  
RA Nakamura S., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,  
RA Okinaga S., Kobayashi T.;  
RT "An endoplasmic reticulum protein, calreticulin, is transported into  
RT the acrosome of rat sperm.";  
RL Exp. Cell Res. 205:101-110(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Sprague-Dawley; TISSUE=Liver;

RX MEDLINE=95181573; PubMed=7876339;  
RA Soennichsen B., Fueillekrug J., van Nguyen P., Diekmann W.,  
RA Robinson D.G., Mieskes G.;  
RT "Retention and retrieval: both mechanisms cooperate to maintain  
RT calreticulin in the endoplasmic reticulum.";  
RL J. Cell Sci. 107:2705-2717(1994).  
RN [4]  
RP SEQUENCE OF 270-358 FROM N.A.  
RC STRAIN-Sprague-Dawley;  
RA Lone Y.C., Bailly A., Latruffe N.;  
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 18-29.  
RX MEDLINE=91054414; PubMed=2241926;  
RA Treves S., de Mattei M., Ianfredi M., Villa A., Green N.M.,  
RA MacLennan D.H., Meldolesi J., Pozzan T.;  
RT "Calreticulin is a candidate for a calsequestrin-like function in  
RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
RL Biochem. J. 271:473-480(1990).  
RN [6]  
RP SEQUENCE OF 18-32.  
RC STRAIN-Sprague-Dawley; TISSUE=Testis;  
RX MEDLINE=92360010; PubMed=1497655;  
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
RT "Calreticulin is present in the acrosome of spermatozoa of rat  
RT testis.";  
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
RN [7]  
RP SEQUENCE OF 18-32.  
RC STRAIN-LEC; TISSUE=Liver;  
RX MEDLINE=94072621; PubMed=8251535;  
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
RA Kamataki T.;  
RT "Identification of protein disulfide isomerase and calreticulin as  
RT autoimmune antigens in LEC strain of rats.";  
RL Biochim. Biophys. Acta 1158:339-344(1993).  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-  
CC HYDROXYBUTYRATE DEHYDROGENASE.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: D78308; BAA11345.1; -;  
DR EMBL: X53363; CAA37446.1; -;  
DR EMBL: X13702; CAA31987.1; ALT\_SEQ.  
DR EMBL: X79327; CAA55890.1; -;  
DR PIR: S04867; S04867.  
DR PIR: S11205; S11205.  
DR PIR: S13045; S13045.  
DR PIR: A49176; A49176.  
DR PIR: S45036; S45036.  
DR PIR: JH0819; JH0819.  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00014; ER\_TARGET; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 17

```
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 266713CED31A2970 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1,7e-55;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFYNGKKNVLIINKDIRCKDEFTHTLTVLRPDNTYEVKIDNSOVESGLE 60
Db 138 GPGTKKVVHVFYNGKKNVLIINKDIRCKDEFTHTLTVLRPDNTYEVKIDNSOVESGLE 197

RESULT 3
CRTC_HUMAN STANDARD: PRT; 417 AA.
ID CRTC_HUMAN
AC P27797;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60).
GN CALR OR CRTC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013129; PubMed=1919005;
RA Rokeach L.A., Haselby J.A., Mello J.F., Smeenk R.J., Unnasch T.R.,
RT Greene B.M., Hoch S.O.,
RL "Characterization of the autoantigen calreticulin.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237213; PubMed=2332496;
RA McCauliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9219342; PubMed=1739953;
RA McCauliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [6]

RP SEQUENCE FROM N.A.
RC TISSUE=Eye, Pancreas, and Skin;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 18-36.
RX MEDLINE=92002034; PubMed=1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866(1991).
RN [8]
RP SEQUENCE OF 18-32.
RX MEDLINE=90380058; PubMed=2400400;
RA Krause K.H., Stimmerman H.R.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RL Biochem. J. 270:545-548(1990).
RN [9]
RP SEQUENCE OF 18-28.
RP TISSUE=Liver;
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Balroch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver proteome map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [10]
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Geeser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [11]
RP SEQUENCE OF 18-26.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Edes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- STIMULANT: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
CC autoantigen.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M84739; AAA51916.1; -
DR EMBL; M32294; AAA36582.1; -
DR EMBL; AY047586; AAL13126.1; -
DR EMBL; AD000092; AAB51176.1; -
DR EMBL; BC002500; AAH02500.1; -
DR EMBL; BC007911; AAH02911.1; -
DR EMBL; BC020493; AAH20493.1; -
DR PIR; A37047; A37047.
DR PIR; S1475; S1475.
DR PIR; A42330; A42330.
DR PIR; A46452; A46452.
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DR SWISS-2DPAGE: P27797; HUMAN.  
 DR Aethus/Ghent-2DPAGE: 9401; IEF.  
 DR PMMA-2DPAGE: P27797; -.  
 DR PHCI-2DPAGE: P27797; -.  
 DR HSC-2DPAGE: P27797; HUMAN.  
 DR Siena-2DPAGE: P27797; -.  
 DR Genew; HGNC:1455; CALR.  
 DR MIM; 109091; -.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 417 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PRESENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-55;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVVHIFMYKGNVYINDKICKDEFTHTLYTPRNTYEVKRTIDNSQVSGSLE 60  
 DB 138 GPGTKKVVHIFMYKGNVYINDKICKDEFTHTLYTPRNTYEVKRTIDNSQVSGSLE 197

RESULT 4  
 CRTC\_RABIT STANDARD; PRT; 418 AA.  
 AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DE 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Slow-twitch skeletal muscle;  
 RX MEDLINE=90094320; PubMed=2600080;  
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;  
 RT "Molecular cloning of the high affinity calcium-binding protein  
 (calreticulin) of skeletal muscle sarcoplasmic reticulum.";  
 RL J. Biol. Chem. 264:21522-21528(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Fast-twitch skeletal muscle;  
 RX MEDLINE=91282795; PubMed=2059224;  
 RA Fliegel L., Michalak M.;

RT "Fast-twitch and slow-twitch skeletal muscles express the same  
 RT isoform of calreticulin.";  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 RN [3]  
 RP SEQUENCE OF 18-36.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [4]  
 RP SEQUENCE OF 18-46.  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Bakesh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RL reticulum.";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE-Lung;  
 RX MEDLINE=92002038; PubMed=1911780;  
 RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 RT monooxygenase and calreticulin.";  
 RL Biochemistry 30:9892-9900(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL; J05138; AAA31188.1; -.  
 DR PIR; A34154; A34154.  
 DR PIR; C33208; C33208.  
 DR PIR; D33208; D33208.  
 DR PIR; E33208; E33208.  
 DR PIR; F33208; F33208.  
 DR PIR; S13046; S13046.  
 DR PIR; S13047; S13047.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 418 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 418 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.

FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 415 418 PREVENT SECRETION FROM ER.  
 FT VARIANT 35 35 E -> D.  
 FT CONFLICT 90 90 P -> T (IN REF. 5).  
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-55;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFYKNGKNNVINKDIRCKDEPHTLTLVPRNFEYKIDNSQVSGSLE 60  
 Db 138 GPGTKKVVHVFYKNGKNNVINKDIRCKDEPHTLTLVPRNTEYKIDNSQVSGSLE 197

## RESULT 5

CRT1\_BOVIN STANDARD; PRT; 400 AA.  
 AC P52193;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).  
 OS Bos taurus (bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RA MEDLINE=94183174; PubMed=8135753;  
 RX Matsuno K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;  
 RL "Covalent structure of bovine brain calreticulin.";  
 RL Biochem. J. 298:435-442(1994).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.  
 FT DOMAIN 1 180 N-DOMAIN.  
 FT CHAIN 181 291 P-DOMAIN.  
 FT DOMAIN 292 400 C-DOMAIN.  
 FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.  
 FT REPEAT 174 185 1-1.  
 FT REPEAT 193 204 1-2.  
 FT REPEAT 204 221 1-3.  
 FT REPEAT 221 238 1-4.  
 FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.  
 FT REPEAT 242 252 2-1.  
 FT REPEAT 252 266 2-2.  
 FT REPEAT 266 270 2-3.  
 FT REPEAT 270 280 2-3.  
 FT DOMAIN 334 390 ASP/GLU/LYS-RICH.  
 FT DISULFID 120 146  
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 397 400 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;

Query Match 68.3%; Score 41; DB 1; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-35;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFYKNGKNNVINKDIRCKDEPHTLTLVPR 41  
 Db 121 GPGTKKVVHVFYKNGKNNVINKDIRCKDEPHTLTLVPR 161

## RESULT 6

CRT2\_BOVIN STANDARD; PRT; 421 AA.  
 ID CRT2\_BOVIN  
 AC P42918;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Calreticulin, brain isoform 2 precursor (CRP55) (calregulin) (HACBP).  
 OS Bos taurus (bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93385184; PubMed=8373827;  
 RA Liu N., Fine R.E., Johnson R.J.;  
 RL "Comparison of cDNAs from bovine brain coding for two isoforms of  
 RL calreticulin.";  
 RL Biochim. Biophys. Acta 1202:70-76(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL: L13462; AAC37307.1; .  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 34 POTENTIAL.  
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.  
 FT DOMAIN 35 201 N-DOMAIN.  
 FT DOMAIN 202 312 P-DOMAIN.  
 FT DOMAIN 313 421 C-DOMAIN.  
 FT REPEAT 313 421 4 X APPROXIMATE REPEATS.  
 FT REPEAT 313 325 1-1.  
 FT REPEAT 325 338 1-2.  
 FT REPEAT 338 351 1-3.  
 FT REPEAT 351 364 1-4.  
 FT REPEAT 364 377 2-1.  
 FT REPEAT 377 390 2-2.  
 FT REPEAT 390 403 2-3.  
 FT REPEAT 403 416 2-3.  
 FT DOMAIN 417 421 ASP/GLU/LYS-RICH.  
 FT DISULFID 141 167 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 PREVENT SECRETION FROM ER.  
 FT SITE 418 421  
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 68.3%; Score 41; DB 1; Length 421;

Best Local Similarity 100.0%; Pred. No. 1.4e-35;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKRVHVFNNKGNVLINKDIRCKDDEFTLHYTLIVRP 41  
142 GPGTKRVHVFNNKGNVLINKDIRCKDDEFTLHYTLIVRP 182

## RESULT 7

CRTC\_SCHMA STANDARD; PRT; 393 AA.  
AC 006814; 026562;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Calreticulin precursor (SM4 protein).  
OS Schistosoma mansoni (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_Taxid=6183;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=Puerto Rican;  
RX MEDLINE=93165070; PubMed=8433712;  
RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,  
RA Capron A.;  
RT "Cloning of the gene encoding a Schistosoma mansoni antigen  
RT homologous to human Ro/SS-A autoantigen.";  
RT Mol. Biochem. Parasitol. 57:193-202(1993).  
RN 12  
RP SEQUENCE FROM N.A.  
RC STRAIN=Puerto Rican;  
RX MEDLINE=94187805; PubMed=8139623;  
RA Khalife J., Pierce R.J., Godin C., Capron A.;  
RT "Cloning and sequencing of the gene encoding Schistosoma mansoni  
RT calreticulin.";  
RT Mol. Biochem. Parasitol. 62:313-315(1993).  
RN 13  
RP FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
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RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Gibbs R.A., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA "The genome sequence of Drosophila melanogaster."
RA Science 287:2185-2195(2000).
RL [3]
RN
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE=90307981; PubMed=2365822;
RA McCauliffe D.P., Zappi E., Lieu T.S., Michalak M., Southeimer R.D.,
RA Capra J.D.;
RA "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RT highly homologous with onchocercal RAL-1 antigen and an alysia
RT 'memory molecule'."
RL J. Clin. Invest. 86:332-335(1990).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X64461; CAA45791.1; -.
CC DR EMBL: AE003683; AAF54416.1; -.
CC DR PIR: A37158; A37158.
CC DR FLYBase: FBgn0005585; Crc.
CC DR InterPro: IPR001580; Calreticulin.
CC DR InterPro: IPR000886; ER_target.
CC DR Pfam: PF00262; Calreticulin; 1.
CC DR PRINTS: PR00626; CALRETICULIN.
CC DR PRODOM: PD001866; Calreticulin; 1.
CC DR PROSITE: PS00014; ER_TARGET; 1.
CC DR PROSITE: PS00803; CALRETICULIN_1; 1.
CC DR PROSITE: PS00804; CALRETICULIN_2; 1.
CC DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
CC KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC FT SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 406 CALRETICULIN.
CC FT CONFLICT 107 107 G -> A (IN REF. 3).
CC FT CONFLICT 184 184 V -> L (IN REF. 3).
CC FT FT
CC SQ SEQUENCE 406 AA; 46808 MM; 65D72C69D0BEC427 CRC64;
Query Match 21.7%; Score 13; DB 1; Length 406;
Best Local Similarity 100.0%; Pred. NO. 2.9e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 YTLIVRPDNTYEV 47
DB 172 YTLIVRPDNTYEV 184

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RX MEDLINE=94341871; PubMed=7520419;
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
RA "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis."
RT Infect. Immun. 62:3696-3704(1994).
RN [2]
RN
RP SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE=88273584; PubMed=2455736;
RA Unasch T.R., Gallin M.T., Soboslay P.T., Ettmann K.D., Greene B.M.;
RA "Isolation and characterization of expression cDNA clones encoding
RT antigens of Onchocerca volvulus infective larvae."
RT J. Clin. Invest. 82:262-269(1988).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M20565; AAA59056.1; -.
CC DR PIR: A32507; A32507.
CC DR InterPro: IPR001580; Calreticulin.
CC DR Pfam: PF00262; Calreticulin; 1.
CC DR PRINTS: PR00626; CALRETICULIN.
CC DR PRODOM: PD001866; Calreticulin; 1.
CC DR PROSITE: PS00803; CALRETICULIN_1; 1.
CC DR PROSITE: PS00804; CALRETICULIN_2; 1.
CC DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
CC KW Calcium-binding; Repeat; Antigen; Signal.
CC FT SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 388 RAL-1 PROTEIN.
CC FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
CC FT REPEAT 189 200 1-1.
CC FT REPEAT 208 219 1-2.
CC FT REPEAT 225 236 1-3.
CC FT REPEAT 242 253 1-4.
CC FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
CC FT REPEAT 257 267 2-1.
CC FT REPEAT 271 281 2-2.
CC FT REPEAT 285 295 2-3.
CC FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
CC FT DISULFD 135 161 BY SIMILARITY.
CC SQ SEQUENCE 388 AA; 45298 MM; 9537F298A2D31CD6 CRC64;
Query Match 18.3%; Score 11; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. NO. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPGTKKHVYIF 11
DB 136 GPGTKKHVYIF 146

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RESULT 9
RAL1_ONCVO STANDARD: PRT; 388 AA.
ID RAL1_ONCVO STANDARD: PRT; 388 AA.
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 protein precursor (41 kDa larval antigen).
GN RAL1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.

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RESULT 10
CRTC_CAEEL STANDARD: PRT; 395 AA.
ID CRTC_CAEEL STANDARD: PRT; 395 AA.
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
DE CRTC-1 OR Y38A10A.5.
GN Caenorhabditis elegans.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-Bristol N2;

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RX MEDLINE=92329978; PubMed=1627827;
RA Smith M.J.;
RA "A.C. elegans gene encodes a protein homologous to mammalian
RT calreticulin.";
RL DNA Seq. 2:235-240(1992).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Bauer C., Courtney L., Laplant Y.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@sdb.ch).
CC -----
DR EMBL; X59589; CAA42159.1; -.
DR EMBL; AF125963; AAD14746.1; -.
DR PIR; S25851; S25851.
DR Wormpep; X38A10A.5; CE21562.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000866; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 15
FT CHAIN 16 395
FT DOMAIN 7 192
FT DOMAIN 193 301
FT DOMAIN 302 395
FT DOMAIN 186 250
FT REPEAT 186 197
FT REPEAT 205 216
FT REPEAT 222 233
FT REPEAT 239 250
FT REPEAT 254 292
FT DOMAIN 254 264
FT REPEAT 268 278
FT REPEAT 282 292
FT DOMAIN 332 390
FT SIGNAL 133 158
FT SITE 392 395
SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;

Query Match
Best Local Similarity 15.0%; Score 9; DB 1; Length 395;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 DNTYEKID 50
DB 174 DNTYEKID 182

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DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Chromosomal protein Mcl (HMB).
OS Methanosarcina barkeri.
OC Archaea: Euryarchaeota: Methanococci: Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2208;
RN [1]
RN SEQUENCE.
RC STRAIN=MS / DSM 800;
RX MEDLINE=87080318; PubMed=3098561;
RA Laine B., Chartier F., Imbert M., Lewis R., Sautiere P.;
RT "Primary structure of the chromosomal protein Hmb from the
RL archaeobacteria Methanosarcina barkeri.";
RN Eur. J. Biochem. 161:681-687(1986).
RN [2]
RN CONFORMATIONAL STUDIES.
RX MEDLINE=90254162; PubMed=2111171;
RA Imbert M., Laine B., Helbecque N., Mornon J.-P., Henlehart J.-P.,
RA Sautiere P.;
RT "Conformational study of the chromosomal protein Mcl from the
RL archaeobacterium Methanosarcina barkeri.";
RX Biochim. Biophys. Acta 1038:346-354(1990).
CC -1- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES
CC TRANSCRIPTION.
DR PIR; A25343; A25343.
DR PIR; S13716; S13716.
KW DNA-binding.
SQ SEQUENCE 93 AA; 10755 MW; 3B5E17405CE2171C CRC64;

Query Match
Best Local Similarity 11.7%; Score 7; DB 1; Length 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GTRKVVH 9
DB 51 GTRKVVH 57

RESULT 12
HMC1_METTE STANDARD; PRT; 93 AA.
ID HMC1_METTE
AC P12770;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Chromosomal protein Mcl.
OS Methanosarcina thermophila.
OC Archaea: Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2210;
RN [1]
RN SEQUENCE.
RC STRAIN=CHT 55 / DSM 2902;
RX MEDLINE=89335731; PubMed=2503033;
RA Chartier F., Laine B., Belaine D., Touzel J.-P., Sautiere P.;
RT "Primary structure of the chromosomal protein Mcl from the
RL archaeobacterium Methanosarcina sp. CHTI 55.";
RX Biochim. Biophys. Acta 1008:309-314(1989).
CC -1- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES
CC TRANSCRIPTION.
DR PIR; S05243; S05243.
DR PIR; S13712; S13712.
KW DNA-binding.
SQ SEQUENCE 93 AA; 10663 MW; 294AA187BD549C28 CRC64;

Query Match
Best Local Similarity 11.7%; Score 7; DB 1; Length 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GTRKVVH 9
DB 51 GTRKVVH 57

```

Db 51 GTRKAVH 57

RESULT 13

RPAA2\_PVRAB STANDARD; PRT; 397 AA.

AC Q9V113;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).

GN RPOA2 OR PAB0425.

OS Pyrococcus abyssi.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.

OX NCBI\_TaxID=29292;

RP SEQUENCE FROM N.A.

RC STRAIN=GES / Orsay;

RA Hellig R.;

RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

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CC EMBL: AJ248284; CAB49538.1; -

DR InterPro: IPR002879; RNA\_POL\_A2.

DR Pfam: PF01854; RNA\_POL\_A2; 1.

KW Transferase; Transcription; DNA-directed RNA polymerase; Complete proteome.

SO SEQUENCE 397 AA; 44594 MW; E459658EAE9C15CB CRC64;

Query Match 11.7%; Score 7; DB 1; Length 397;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 YTLVIRP 41

Db 198 YTLVIRP 204

RESULT 14

RPAA2\_PVRFU STANDARD; PRT; 397 AA.

AC Q8U0M5;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).

GN RPOA2 OR PFI562.

OS Pyrococcus furiosus.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.

OX NCBI\_TaxID=2261;

RP SEQUENCE FROM N.A.

RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;

RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

RT "The complete sequence of the Pyrococcus furiosus genome."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

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CC EMBL: AE010257; ALA81686.1; -

DR Transferase; Transcription; DNA-directed RNA polymerase; Complete proteome.

KW SEQUENCE 397 AA; 44404 MW; 19D46E356CA0E49F CRC64;

SO

Query Match 11.7%; Score 7; DB 1; Length 397;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 YTLVIRP 41

Db 198 YTLVIRP 204

RESULT 15

RPAA2\_PVRHO STANDARD; PRT; 397 AA.

AC Q93777;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).

GN RPOA2 OR PHI544.

OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.

OX NCBI\_TaxID=53953;

RP SEQUENCE FROM N.A.

RC STRAIN=OT3;

RA MEDLINE=98344137; PubMed=9679194;

RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otuka R., Nakazawa H., Takamya M., Ohfuku A., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;

RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."

RL DNA Res. 5:55-76(1998).

CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

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CC EMBL: AP000006; BAA30655.1; -

DR InterPro: IPR002879; RNA\_POL\_A2.

DR Pfam: PF01854; RNA\_POL\_A2; 1.

KW Transferrase; Transcription; DNA-directed RNA polymerase;  
 KW Complete proteome.  
 SQ SEQUENCE 397 AA; 44507 MM; 784655AB5D4730D CRC64;

Query Match 11.7%; Score 7; DB 1; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 YTLIVRP 41  
 |||||  
 Db 198 YTLIVRP 204

Search completed: March 14, 2003, 20:45:09  
 Job time : 3.29226 secs

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 4.29799 Seconds

(without alignments)  
1342.037 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60  
Sequence: 1 GPGTKKVVHVFYKGNVLI.....PNTYEKIDNSQVESGSLE 60Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	416	1 S06763	calreticulin precu
2	60	100.0	416	2 JH0819	calreticulin precu
3	60	100.0	417	1 A37047	calreticulin precu
4	60	100.0	418	1 A34154	calreticulin precu
5	41	68.3	400	2 S43376	calreticulin, bral
6	41	68.3	421	2 S36799	calreticulin, bral
7	22	36.7	384	2 S29130	calreticulin precu
8	22	36.7	411	2 S29129	calreticulin (clon
9	20	33.3	419	2 S71343	calreticulin precu
10	19	31.7	405	1 JH0795	calreticulin precu
11	14	23.3	393	1 A48573	calreticulin precu
12	13	21.7	406	2 A56637	calreticulin autoa
13	11	18.3	336	2 A32507	calreticulin homol
14	9	15.0	395	2 S25851	41K larval antigen
15	7	11.7	93	2 A25343	calreticulin precu
16	7	11.7	93	2 S05243	nonhistone chromos
17	7	11.7	93	2 S13717	histone-like prote
18	7	11.7	358	2 T12850	hypothetical prote
19	7	11.7	397	2 G75182	DNA-directed RNA p
20	7	11.7	397	2 G71031	probable DNA-direc
21	7	11.7	414	2 T39450	phosphoglycerate k
22	7	11.7	591	2 B54354	calnexin precursor
23	7	11.7	591	2 C54354	calnexin precursor
24	7	11.7	592	2 I53260	calnexin - human
25	7	11.7	592	2 A46673	calnexin precursor
26	7	11.7	593	1 A37273	calnexin precursor
27	7	11.7	1461	2 E84589	probable retroelem
28	6	10.0	19	2 S54848	succinyl-CoA synth
29	6	10.0	81	2 F97347	transition state r

30	6	10.0	87	2 B34455	methanogen chromos
31	6	10.0	89	2 A34455	methanogen chromos
32	6	10.0	90	2 C34455	methanogen chromos
33	6	10.0	97	2 H69440	ribosomal protein
34	6	10.0	103	2 F75010	hypothetical prote
35	6	10.0	109	2 E64473	DNA-directed RNA p
36	6	10.0	144	2 A96580	hypothetical prote
37	6	10.0	146	2 S66060	yeast protein - Bac
38	6	10.0	152	2 T18975	hypothetical prote
39	6	10.0	160	2 C84279	hypothetical prote
40	6	10.0	173	2 AC3503	nickel-cobalt-cadm
41	6	10.0	187	2 T25461	hypothetical prote
42	6	10.0	196	2 S63429	CIS1 protein - yea
43	6	10.0	203	2 H96525	probable terpene c
44	6	10.0	214	2 I49758	hypoxanthine phosph
45	6	10.0	218	1 RTH0G	

## ALIGNMENTS

```
RESULT 1
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmic; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI444; PC1233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
A:Reference number: S06763; M0ID:90059955; PMID:2563110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMI>
A:Cross-references: EMBL:X14926; NID:950567; PIDN:CAA33053.1; PID:950568
R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca
A:Reference number: JCI444; M0ID:93013037; PMID:1398135
A:Accession: JCI444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MAZ>
R:White, T.K.; Zhu, O.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mous
A:Reference number: A57498; M0ID:95332280; PMID:7608143
A:Accession: A57498
A>Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 60; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 7;le-56;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFYKGNVLIINKDKDEFTHTLTVRPNMTYEKIDNSQVESGSLE 60
Db 138 GPGTKKVVHVFYKGNVLIINKDKDEFTHTLTVRPNMTYEKIDNSQVESGSLE 197

RESULT 2
JH0819
calreticulin precursor - rat
```

N:Alternate names: calcium-binding protein 3  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000  
 A:Accession: J00819; A49176; S11205; P01109; S45036; S39372; A34473; S13045  
 R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.  
 Exp. Cell Res. 205, 101-110, 1993  
 A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom  
 A:Reference number: A49176; MUID:93202172; PMID:8453984  
 A:Accession: J00819  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <NAK>  
 A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572  
 A:Accession: A49176  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-416 <NA2>  
 A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572  
 A:Experimental source: Sprague-Dawley, spermatogenic cells  
 A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBI:P127643)  
 R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y  
 Nucleic Acids Res. 18, 4933, 1990  
 A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc  
 A:Reference number: S11205; MUID:90370496; PMID:2395661  
 A:Accession: S11205  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <MUR>  
 A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855  
 R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
 A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.  
 A:Reference number: P01109; MUID:92360010; PMID:1497655  
 A:Accession: P01109  
 A:Molecule type: protein  
 A:Residues: 18-32 <NAK2>  
 A:Experimental source: testis, strain Sprague-Dawley  
 R:Schonlichsen, B.; Fuenflekner, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes  
 submitted to the EMBL Data Library, May 1994  
 A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul  
 A:Reference number: S45036  
 A:Accession: S45036  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <SOE>  
 A:Cross-references: EMBL:X79327; NID:g48840; PIDN:CAA55890.1; PID:g48841  
 R:Lione, Y.C.; Bailly, A.; Lalruite, N.  
 submitted to the EMBL Data Library, December 1988  
 A:Reference number: S04867  
 A:Accession: S04867  
 A:Molecule type: mRNA  
 A:Residues: R', 270-358, 'AAG' <LON>  
 A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260  
 A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
 R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.  
 Biochim. Biophys. Acta 1158, 339-344, 1993  
 A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmu  
 A:Reference number: S39371; MUID:94072621; PMID:8251535  
 A:Accession: S39372  
 A:Molecule type: protein  
 A:Residues: 18-23, 'X', 25-32 <YOK>  
 R:Van, P.N.; Peter, F.; Soelling, H.D.  
 J. Biol. Chem. 264, 17494-17501, 1989  
 A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wi  
 tive calcium sequestering rat liver vesicles.  
 A:Reference number: A34473; MUID:90008920; PMID:2793869  
 A:Accession: A34473  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-36 <VAN>  
 R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
 Biochem. J. 271, 473-480, 1990  
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
 A:Reference number: S13045; MUID:91054414; PMID:2241926  
 A:Accession: S13045

A:Molecule type: protein  
 A:Residues: 18-29 <TRE>  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding; glycoprotein  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-416/Product: calreticulin #status experimental <MAT>  
 F:204-212/Region: nuclear location signal  
 F:413-416/Region: endoplasmic reticulum retention signal  
 F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 60; DB 2; Length 416;  
 Best Local Similarity 100.0%; Pred. NO. 7.1e-56;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKVHVFYFKGNVLINCKDKDEPHLYTLVLPDNTYEKIDNSQVSGSL 60  
 DB 138 GGTGKVVHVFYFKGNVLINCKDKDEPHLYTLVLPDNTYEKIDNSQVSGSL 197

RESULT 3  
 A37047  
 calreticulin precursor - human

N:Alternate names: 52k ribonucleoprotein autoantigen Ro/SS-A; 60k integrin-binding pr  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
 A:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
 R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sonthelmer, R.D.; Capra, J.D.  
 J. Biol. Chem. 267, 2557-2562, 1992  
 A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
 A:Reference number: A42330; MUID:92129342; PMID:1733953  
 A:Accession: A42330  
 A:Molecule type: DNA  
 A:Residues: 1-417 <MC2>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:P78536)  
 R:McCaulliffe, D.P.; Lux, F.A.; Lien, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
 J. Clin. Invest. 85, 1379-1391, 1990  
 A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
 A:Reference number: A37047; MUID:90237213; PMID:2332496  
 A:Accession: A37047  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <MCC>  
 A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA56582.1; PID:g337487  
 A:Note: the authors translated the codon GTA for residue 349 as Tyr  
 R:Roheach, U.A.; Haselby, J.A.; Melilot, J.F.; Smeene, R.J.; Unnasch, T.R.; Greene, B.  
 J. Immunol. 147, 3031-3039, 1991  
 A:Title: Characterization of the autoantigen calreticulin.  
 A:Reference number: A46452; MUID:92013129; PMID:1919005  
 A:Accession: A46452  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <ROR>  
 A:Cross-references: GB:M64739; NID:g179881; PIDN:AAA51916.1; PID:g179882  
 A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBI:P60750)  
 R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sonthelmer, R.D.  
 J. Clin. Invest. 82, 96-101, 1988  
 A:Title: Molecular characterization of the human Ro/SS-A antigen. Amino terminal sequence  
 A:Reference number: A28812; MUID:88273610; PMID:3260607  
 A:Accession: A28812  
 A:Molecule type: protein  
 A:Residues: 18-41 <LIE>  
 A:Note: 18-Ala was also found  
 R:Dupuis, M.; Scherer, E.; Krause, K.H.; Tschopp, J.  
 J. Exp. Med. 177, 1-7, 1993  
 A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
 A:Reference number: PH1525; MUID:93115648; PMID:8418194  
 A:Accession: PH1525  
 A:Molecule type: protein  
 A:Residues: 18-27 <DUP>  
 A:Experimental source: LAK cell  
 R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Deghar, S.  
 Biochemistry 30, 9859-9866, 1991  
 A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (C  
 A:Reference number: A40346; MUID:92002034; PMID:1911778  
 A:Accession: A40346

A:Molecule type: protein  
A:Residues: 18-34, 'R' <ROJ>  
R: Krause, K.H.; Sliemers, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the ER chaperone BiP  
A:Reference number: S11475; MUID:90380058; PMID:2400400  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R: Lamerlin, J.; McCready, P.; Stillwagen, S.; Ramlier, M.; Carrano, A.  
Submitted to the EMBL Data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region  
A:Reference number: 222906  
A:Accession: T45075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAW>  
A:Cross-references: EMBL:AD000092; PIDN:AA51176.1  
A:Experimental source: cell line 5HL2-B; fibroblast  
A:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and Celiac disease  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3  
A:Note: CIRC  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <MAT>  
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 60; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 7.1e-56;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GPGTKVHVIIFYNKGKKNVILNKDICKDEFTHTLTLVPRDNTYEKIDNSQVSGSLE 60  
Db 138 GPGTKVHVIIFYNKGKKNVILNKDICKDEFTHTLTLVPRDNTYEKIDNSQVSGSLE 197

RESULT 4  
A34154  
calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34154; S13047  
R: Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA from rabbit skeletal muscle  
A:Reference number: A34154; MUID:90094320; PMID:2600080  
A:Accession: A34154  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <FLU>  
A:Cross-references: GB:J05138; NID:g164858; PIDN:AA31188.1; PID:g164859  
R: Treves, S.; de Mattei, M.; Lanfretti, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A:Reference number: S13045; MUID:91054414; PMID:2241926  
A:Accession: S13047  
A:Molecule type: protein  
A:Residues: 19-32 <TRB>  
C:Superfamily: calreticulin  
C:Keywords: skeletal muscle  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 60; DB 1; Length 418;  
Best Local Similarity 100.0%; Pred. No. 7.1e-56;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GPGTKVHVIIFYNKGKKNVILNKDICKDEFTHTLTLVPRDNTYEKIDNSQVSGSLE 60

Db 138 GPGTKVHVIIFYNKGKKNVILNKDICKDEFTHTLTLVPRDNTYEKIDNSQVSGSLE 197  
RESULT 5  
S43376  
calreticulin, brain isoform 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
C:Accession: S43376; S36801  
R: Matsuka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
Biochem. J. 298, 435-442, 1994  
A:Title: Covalent structure of bovine brain calreticulin  
A:Reference number: S43376; MUID:94183174; PMID:8135753  
A:Accession: S43376  
A:Molecule type: protein  
A:Residues: 1-400 <MAT>  
A:Experimental source: brain  
R: Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin  
A:Reference number: S36799; MUID:93385184; PMID:8373827  
A:Accession: S36801  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 45-63, 'E', 65-83 <LTI>  
A:Experimental source: brain, clone 8.1  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:397-400/Region: endoplasmic reticulum retention signal  
F:120-146/Disulfide bonds: #status experimental  
F:162/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 68.3%; Score 41; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 1e-35;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKVHVIIFYNKGKKNVILNKDICKDEFTHTLTLVPR 41  
Db 121 GPGTKVHVIIFYNKGKKNVILNKDICKDEFTHTLTLVPR 161

RESULT 6  
S36799  
calreticulin precursor, brain isoform 2 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 13-Aug-1999  
C:Accession: S36799; S36800  
R: Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin  
A:Reference number: S36799; MUID:93385184; PMID:8373827  
A:Accession: S36799  
A:Molecule type: mRNA  
A:Residues: 1-421 <LTI>  
A:Cross-references: GB:J13462; NID:g348693; PIDN:AA37307.1; PID:g348694  
A:Experimental source: brain, clone 9.4  
A:Accession: S36800  
A:Molecule type: protein  
A:Residues: 35-45 <LTI>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>  
F:418-421/Region: endoplasmic reticulum retention signal  
F:141-167/Disulfide bonds: #status predicted  
F:183/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 68.3%; Score 41; DB 2; Length 421;  
Best Local Similarity 100.0%; Pred. No. 1.1e-35;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GPGTKVHVIIFYNKGKKNVILNKDICKDEFTHTLTLVPR 41

```
|||||
DB 142 GPGTKKVVHFMKGNVILNKDIRCKDDEFHLYTLIVRP 182

RESULT 7
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TRW>
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.7%; Score 22; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 FTHLYTLIVRPDNTYEKIDNS 52
|||||
DB 140 FTHLYTLIVRPDNTYEKIDNS 161

RESULT 8
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TR>
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.7%; Score 22; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 FTHLYTLIVRPDNTYEKIDNS 52
|||||
DB 163 FTHLYTLIVRPDNTYEKIDNS 184

RESULT 9
S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
```

```
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BA011425.1; PID:g1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 33.3%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTLIVRPDNTYEKIDNS 52
|||||
DB 171 HLYTLIVRPDNTYEKIDNS 190

RESULT 10
JH0795
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calretic
A:Reference number: JH0795; MUID:93098937; PMID:1463604
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:Cross-references: GB:S51239; NID:g262053; PIDN:AA824569.1; PID:g262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion
A:Reference number: A94207; MUID:88320566; PMID:3413132
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified an
A:Reference number: A60977; MUID:89276264; PMID:2731514
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 31.7%; Score 19; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTLIVRPDNTYEKIDN 51
|||||
DB 166 HLYTLIVRPDNTYEKIDN 184

RESULT 11
```



A48573  
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)  
C:Species: Schistosoma mansoni  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48573  
R:Kallite, J.; Trottelen, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.  
Mol. Biochem. Parasitol. 57, 193-202, 1993  
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human  
A:Reference number: A48573; MUID:93165070; PMID:8433712  
A:Accession: A48573  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-393 <KHA>  
A:Cross-references: GB:M93097; NID:g160928  
A:Note: sequence inconsistent with the nucleotide translation  
C:Superfamily: calreticulin  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 23.3%; Score 14; DB 1; Length 393;  
Best local similarity 100.0%; Pred. No. 4.7e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TKKVVHIFNYKGN 17  
|||||  
Db 139 TKKVVHIFNYKGN 152

RESULT 12  
A56637  
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)  
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog  
C:Species: Drosophila melanogaster  
C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
C:Accession: A56637; A37158  
R:Smith, M.J.  
DNA Seq. 3, 247-250, 1992  
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin  
A:Reference number: A56637; MUID:93208374; PMID:1296819  
A:Accession: A56637  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-406 <SMI>  
A:Cross-references: GB:X6461; NID:g7685; PIDN:CAA5791.1; PID:g7686  
A:Note: sequence extracted from NCBI backbone (NCBI:128274, NCBI:128275)  
R:McCaulliffe, D.P.; Zapf, E.; Lien, T.S.; Michalak, M.; Sonthelmer, R.D.; Capra, J.D.  
J. Clin. Invest. 86, 332-335, 1990  
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom  
A:Reference number: A37158; MUID:90307981; PMID:2365822  
A:Accession: A37158  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: DNA  
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'U', 185-220 <MCC>  
A:Gene: FlyBase:Crc  
A:Cross-references: FlyBase:FBgn0005585  
A:Introns: 65/1; 222/3  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 21.7%; Score 13; DB 2; Length 406;  
Best local similarity 100.0%; Pred. No. 5.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 YTLIVRPNTYEV 47  
|||||  
Db 172 YTLIVRPNTYEV 184

RESULT 13

A32507  
41K larval antigen - nematode (Onchocerca volvulus) (fragment)  
C:Species: Onchocerca volvulus  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 12-Apr-1995  
C:Accession: A32507; A28813  
R:Runasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.  
J. Clin. Invest. 82, 262-269, 1988  
A:Title: Isolation and characterization of expression cDNA clones encoding antigens o  
A:Reference number: A92769; MUID:88273584; PMID:2455736  
A:Accession: A32507  
A:Molecule type: mRNA  
A:Residues: 1-336 <UNN>  
C:Superfamily: calreticulin

Query Match 18.3%; Score 11; DB 2; Length 336;  
Best local similarity 100.0%; Pred. No. 0.00063;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVVHIF 11  
|||||  
Db 84 GPGTKKVVHIF 94

RESULT 14  
S25851  
calreticulin precursor - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S25851; T33996  
R:Smith, M.J.  
DNA Seq. 2, 235-240, 1992  
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.  
A:Reference number: S25851; MUID:92329978; PMID:1627827  
A:Accession: S25851  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <SMI>  
A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694  
R:Baier, C.; Courtney, L.; Lapiant, Y.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid Y38A10A.  
A:Reference number: Z21453  
A:Accession: T33996  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-395 <BAU>  
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5  
A:Experimental source: strain Bristol N2; clone Y38A10A  
C:Genetics:  
A:Gene: CESP:Y38A10A.5  
A:Map position: 5  
A:Introns: 107/3; 315/3  
C:Superfamily: calreticulin  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 15.0%; Score 9; DB 2; Length 395;  
Best local similarity 100.0%; Pred. No. 0.096;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 DNTYEVKID 50  
|||||  
Db 174 DNTYEVKID 182

RESULT 15  
A25343  
nonhistone chromosomal protein Hmb - Methanosarcina barkeri  
C:Species: Methanosarcina barkeri  
C:Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 16-Feb-1997  
C:Accession: A25343  
R:Latine, B.; Chartier, F.; Imbert, M.; Lewis, R.; Sautiere, P.  
Eur. J. Biochem. 161, 681-687, 1986

A:Title: Primary structure of the chromosomal protein Hmb from the archaebacteria Methan  
A:Reference number: A25343; MUID:87080318; PMID:3098561  
A:Accession: A25343  
A:Molecule type: Protein  
A:Residues: 1-93 <LAI>  
C:Superfamily: methanogen chromosomal protein  
C:Keywords: chromosomal protein; DNA binding

Query Match 11.7%; Score 7; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GTRKVVHV 9  
|||||||  
Db 51 GTRKVVHV 57

Search completed: March 14, 2003, 20:49:02  
Job time : 5.29799 secs

GenCore version 5.1.4-p5.4578  
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OW protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 10.2006 Seconds  
(without alignments)  
783.783 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60  
Sequence: 1 GPGRKRVHVFNYKGNVLI.....PDNTYEKIDNSQVSGSLE 60

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A\_Geneseq\_101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	21	AAV92354
2	60	100.0	61	21	AAV92352
3	60	100.0	180	21	AAV92351
4	60	100.0	280	21	AAV92355
5	60	100.0	400	21	AAV92350
6	60	100.0	401	18	AAV11156
7	60	100.0	417	10	AAV92276
8	60	100.0	417	20	AAV00927
9	60	100.0	417	21	AAV92349
10	60	100.0	417	23	AAE24591

11	60	100.0	417	23	AAU77712
12	60	100.0	417	23	AAE18851
13	49	81.7	49	21	AAV92353
14	36	60.0	122	20	AAV00924
15	36	60.0	122	20	AAV00926
16	19	31.7	122	20	AAV00925
17	17	28.3	403	17	AAW04171
18	13	21.7	177	23	ABP42414
19	13	21.7	406	22	ABE64410
20	12	20.0	12	23	AAE18840
21	11	18.3	336	12	AAE12312
22	9	15.0	9	19	AAW76264
23	8	13.3	8	19	AAW76265
24	8	13.3	385	21	AAE32385
25	7	11.7	400	22	AAE96198
26	7	11.7	591	22	ABE44553
27	7	11.7	592	22	ABE44554
28	7	11.7	593	16	AAE71094
29	7	11.7	1009	23	AAO20949
30	7	11.7	1090	22	AAE95857
31	7	11.7	1394	22	ABE22611
32	6	10.0	15	20	AAV30496
33	6	10.0	15	20	AAV30499
34	6	10.0	15	20	AAV30500
35	6	10.0	15	20	AAV30501
36	6	10.0	15	20	AAV30504
37	6	10.0	15	20	AAV30505
38	6	10.0	15	20	AAV30509
39	6	10.0	33	22	ABG04480
40	6	10.0	46	22	ABG19823
41	6	10.0	62	20	AAV01421
42	6	10.0	64	22	AAO13737
43	6	10.0	69	23	ABP40517
44	6	10.0	70	20	AAE60500
45	6	10.0	74	23	ABP39970

#### ALIGNMENTS

RESULT 1	AAV92354	standard; Protein: 60 AA.
ID	AAV92354	
AC	AAV92354	
XX		
XX		
DT	10-AUG-2000	(first entry)
XX		
DE	Recombinant human calreticulin residues 121-180.	
XX		
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;	
KW	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;	
KW	cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;	
KW	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
PN	WO200020577-A1.	
XX		
PD	13-APR-2000.	
XX		
PF	05-OCT-1999;	99WO-US23240.
XX		
PR	06-OCT-1998;	98US-0103438.
XX		
PA	(USSS ) US DEPT HEALTH & HUMAN SERVICES.	
XX		
PI	Tosato G, Pike SE, Yao L;	
XX		
DR	WPI; 2000-303767/26.	
XX		
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin,	

PT useful for suppressing tumor growth

XX

PS Claim 4; Page 85; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

CC Kaposi's sarcoma (claimed).

CC

XX

SQ Sequence 60 AA;

Query Match 100.0%; Score 60; DB 21; Length 60;

Best Local Similarity 100.0%; Pred. No. 2.3e-62;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKRVHVIENYKGNVLINCKDCKDEFTLTYLIVRPDNTYEVKIDNSQVSGSL 60

DB 1 GPGTKRVHVIENYKGNVLINCKDCKDEFTLTYLIVRPDNTYEVKIDNSQVSGSL 60

RESULT 2

AAV92352

ID AAV92352 standard; Protein; 61 AA.

XX

AC AAV92352;

XX

DT 10-AUG-2000 (first entry)

XX

DE Recombinant human calreticulin residues 120-180.

XX

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

KW cytosolic; dermatological; immunosuppressive; antiinflammatory; hepatic;

KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US23240.

XX

PR 06-OCT-1998; 98US-0103438.

XX

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

DR WPI; 2000-303767/26.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX

PS Claim 4; Page 82-83; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

CC Kaposi's sarcoma (claimed).

CC

XX

SQ Sequence 61 AA;

Query Match 100.0%; Score 60; DB 21; Length 61;

Best Local Similarity 100.0%; Pred. No. 2.3e-62;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKRVHVIENYKGNVLINCKDCKDEFTLTYLIVRPDNTYEVKIDNSQVSGSL 60

DB 2 GPGTKRVHVIENYKGNVLINCKDCKDEFTLTYLIVRPDNTYEVKIDNSQVSGSL 61

RESULT 3

AAV92351

ID AAV92351 standard; Protein; 180 AA.

XX

AC AAV92351;

XX

DT 10-AUG-2000 (first entry)

XX

DE Human vasostatin (calreticulin N-terminal 180 amino acids).

XX

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;

KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;

KW neuroprotective; antidiabetic; cytosolic; dermatological; hepatic;

KW immunosuppressive; antiinflammatory; anti-atherosclerotic;

KW gastrointestinal; anti-arthritis; ophthalmic.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US23240.

XX

PR 06-OCT-1998; 98US-0103438.

XX

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

DR WPI; 2000-303767/26.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX

PS Claim 4; Page 82; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 180 AA;  
Query Match 100.0%; Score 60; DB 21; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6,4e-62;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GPGTKKVVHVFNYKGNVLINKDKDEFFHLYTLVLRPNTYEKVIDNSQVSGSLE 60  
Db 121 GPGTKKVVHVFNYKGNVLINKDKDEFFHLYTLVLRPNTYEKVIDNSQVSGSLE 180  
RESULT 4  
ID AAY92355 standard; Protein: 280 AA.  
XX  
AC AAY92355;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant delta-120 calreticulin.  
XX  
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US23240.  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Tosato G, Pike SE, Yao L;  
XX  
DR WPI: 2000-303767/26.  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
XX useful for suppressing tumor growth  
XX  
PS Claim 4; Page 86; 99pp; English.  
XX  
CC This sequence comprises recombinant human calreticulin (AAY92350)  
CC missing the N-terminal 120 amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The  
CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX

SQ Sequence 280 AA;  
Query Match 100.0%; Score 60; DB 21; Length 280;  
Best Local Similarity 100.0%; Pred. No. 9,8e-62;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GPGTKKVVHVFNYKGNVLINKDKDEFFHLYTLVLRPNTYEKVIDNSQVSGSLE 60  
Db 1 GPGTKKVVHVFNYKGNVLINKDKDEFFHLYTLVLRPNTYEKVIDNSQVSGSLE 60  
RESULT 5  
ID AAY92350 standard; Protein: 400 AA.  
XX  
AC AAY92350;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant human MBP-calreticulin.  
XX  
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US23240.  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Tosato G, Pike SE, Yao L;  
XX  
DR WPI: 2000-303767/26.  
XX  
PR N-PSDB; AAA09346, AAA09347.  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
XX useful for suppressing tumor growth  
XX  
PS Claim 4; Page 80-81; 99pp; English.  
XX  
CC Recombinant human MBP-calreticulin comprises the sequence of human  
CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The  
CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 400 AA;  
Query Match 100.0%; Score 60; DB 21; Length 400;  
Best Local Similarity 100.0%; Pred. No. 1,4e-61;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYFKGKKNVLIINKDIRCKDDEFTHLYTLIVRPNTYEKIDNSQVESGSLE 60  
|||||  
DB 121 GPGTKKVVHVFYFKGKKNVLIINKDIRCKDDEFTHLYTLIVRPNTYEKIDNSQVESGSLE 180

## RESULT 6

ID AAW11156 standard; peptide; 401 AA.

AC AAW11156;

DT 31-MAY-1997 (first entry)

DE Calreticulin.

KW calreticulin; C-domain; restenosis; inhibitor.

OS Homo sapiens.

PN W09636643-A1.

PD 21-NOV-1996.

PE 17-MAY-1996; 96WO-1B00471.

PR 16-MAY-1996; 96US-0649417.

PR 17-MAY-1995; 95US-0442844.

PA (UYAL-) UNIV ALBERTA.

PI Lucas A, Michalak M;

DR WPI; 1997-012036/01.

PT Inhibition of restenosis in patients - using calreticulin or a

PT C-domain polypeptide of calreticulin or a variant with the same

PT activity.

PS Disclosure; Fig 1; 48pp; English.

CC The present sequence is calreticulin. It and a C-domain derived peptide

CC (AAW06736) are useful for treating a patient to inhibit restenosis. The

CC calreticulin-type cpds. are administered either parenterally,

CC intravenously or via a catheter and can target areas of vascular damage

CC to inhibit or prevent restenosis.

XX

SQ Sequence 401 AA;

Query Match 100.0%; Score 60; DB 18; Length 401;

Best Local Similarity 100.0%; Pred. No. 1.4e-61;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYFKGKKNVLIINKDIRCKDDEFTHLYTLIVRPNTYEKIDNSQVESGSLE 60

|||||

DB 121 GPGTKKVVHVFYFKGKKNVLIINKDIRCKDDEFTHLYTLIVRPNTYEKIDNSQVESGSLE 180

## RESULT 7

ID AAP92276 standard; protein; 417 AA.

AC AAP92276;

DT 23-FEB-1990 (first entry)

DE 60 kD Ro (Ro/SSA) antigen.

KW Sjorens syndrome; systemic lupus erythematosus;

OS Synthetic.

PN W08909273-A.

PD 05-OCT-1989.

PF 22-MAR-1989; 89WO-US01213.

PR 22-MAR-1988; 88US-0171634.

PA (TEXA) UNIV OF TEXAS SYST.

PI Sontheimer RD, Capra JD, McCaulliffe DP;

DR WPI; 1989-309537/42.

DR N-PSDB; AAP92276.

PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen

PT - used in immunoassays to detect rheumatic disease

PS Disclosure; Fig 2; 88pp; English.

CC Synthetic peptides corresp. to an epitopic core of Ro antigen are

CC expressed recombinantly to detect autoantibodies, for identification

CC of autoimmune diseases. These epitopes are Aas 24-36, 23-36, 188-209,

CC or 241-255. The peptides may be substd. for ribonucleoprotein particle

CC antigens.

XX

SQ Sequence 417 AA;

Query Match 100.0%; Score 60; DB 10; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.4e-61;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYFKGKKNVLIINKDIRCKDDEFTHLYTLIVRPNTYEKIDNSQVESGSLE 60

|||||

DB 138 GPGTKKVVHVFYFKGKKNVLIINKDIRCKDDEFTHLYTLIVRPNTYEKIDNSQVESGSLE 197

## RESULT 8

ID AAY00927 standard; protein; 417 AA.

AC AAY00927;

DT 28-MAY-1999 (first entry)

DE Calreticulin.

XX C1q and collectin receptor; cC1q binding domain; complement ubiquitin;

XX CUB functionality; inhibitor; complement activation; inflammation;

XX myocardial infarction; brain ischemia; gut ischemia; amyloid plaque;

XX rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;

XX immune complex nephritis; therapy.

OS Homo sapiens.

PN W09907406-A1.

PD 18-FEB-1999.

PE 12-AUG-1998; 98WO-GB02430.

PR 12-AUG-1997; 97GB-0016998.

PA (UYLE-) UNIV LEICESTER.

PI Schwaible W;

DR WPI; 1999-180404/15.

XX Use of a cC1q binding domain - to modulate complement ubiquitin

XX (CUB) functionality.

PS Disclosure; Page 26-27; 31pp; English.

CC This sequence is calreticulin, a homologue of C1q and collectin receptor

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC protein. This sequence is used in the exemplification of the invention.

SO Sequence 417 AA:

Query Match 100.0%; Score 60; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKVHVIFNFKGNVLINCKDDEFTLHYTLIVPDPNTYEKIDNSQVSGSLE 60  
DB 138 GPGTKVHVIFNFKGNVLINCKDDEFTLHYTLIVPDPNTYEKIDNSQVSGSLE 197

RESULT 11  
AAU77712  
ID AAU77712 standard; Protein; 417 AA.

AAU77712;  
05-JUN-2002 (first entry)

Human calreticulin (CRT).  
Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;  
cytostatic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;  
enhanced antigen-specific immune response; cytotoxic T lymphocyte;  
tumour; cancer; cervical cancer.

Homo sapiens.  
WO200212281-A2.

14-FEB-2002.

02-AUG-2001; 2001WO-US24134.

03-AUG-2000; 2000US-222902P.

(UYJO ) UNIV JOHNS HOPKINS.

Wu T, Hung C;

WPI: 2002-257463/30.

N-PSDB; ABK11662.

New nucleic acids encoding a fusion polypeptide comprising an  
endoplasmic reticulum chaperone polypeptide linked to an antigenic  
polypeptide, useful as a vaccine for inducing antigen-specific immune  
responses -  
Disclosure: Page 27; 71pp; English.

The invention describes a nucleic acid molecule (I) encoding a fusion  
polypeptide comprising a first polypeptide domain comprising an  
endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and  
a second polypeptide domain comprising at least one antigenic peptide  
e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as  
a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune  
responses, particularly those mediated by cytotoxic T lymphocytes. The  
nucleic acid and compositions comprising the nucleic acid is also useful  
for inhibiting the growth of tumours and cancers e.g. cervical cancer.  
This is the amino acid sequence of the human calreticulin (CRT), an  
endoplasmic reticulum protein used in the creation of a DNA vaccine.

Sequence 417 AA:

Query Match 100.0%; Score 60; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKVHVIFNFKGNVLINCKDDEFTLHYTLIVPDPNTYEKIDNSQVSGSLE 60  
DB 138 GPGTKVHVIFNFKGNVLINCKDDEFTLHYTLIVPDPNTYEKIDNSQVSGSLE 197

RESULT 12  
AAE18851  
ID AAE18851 standard; Protein; 417 AA.

AAE18851;

17-MAY-2002 (first entry)

Human calreticulin protein.

Human; prostate cancer; calreticulin; T1D-1 protein; TRAIRS protein;  
androgen action pathway; cell proliferation; kidney cancer; lymphoma;  
epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;  
cytostatic; U19 protein.

Homo sapiens.

Location/Qualifiers

Domain /label= N-terminal\_domain

Region /label= Alpha\_helix

Region /label= Alpha\_helix

Domain /label= Alpha\_helix

Domain /note= "Proline-rich domain (P domain)"

Domain /label= C-terminal\_domain

WO200206327-A2.

24-JAN-2002.

17-JUL-2001; 2001WO-US22357.

17-JUL-2000; 2000US-218761P.

16-JUL-2001; 2001US-0906393.

(NOUN ) UNIV NORTHWESTERN.

Wang Z, Xiao W;

WPI: 2002-179780/23.

N-PSDB; AAD29931.

Identifying a subject that is likely to have aggressive form of  
prostate cancer, involves comparing calreticulin levels in prostate  
specimen of the subject and in benign prostatic epithelial cells of the  
same subject -  
Disclosure: Page 146-148; 148pp; English.

The present invention relates to methods of distinguishing aggressive  
forms of prostate cancer from non-aggressive forms. The method involves  
comparing the level of calreticulin in prostate specimen and in benign  
prostatic epithelial cells of a subject. The invention particularly  
relates to two proteins, namely calreticulin and T1D-1 (TRAIRS; U19)  
that are down-regulated in aggressive forms of prostate cancer but not  
in slowly progressing prostate cancer. They play important roles in  
the part of androgen action pathway that suppresses cell proliferation  
and/or prevents prostate cancer. The method is useful for identifying  
a subject who is likely to have an aggressive form of prostate cancer.  
The invention further relates to a method of identifying a subject with  
a slow growing form of prostate cancer. T1D-1 sequences are useful for  
treating cancers such as epithelium-derived carcinomas, kidney cancers,  
lymphomas, leukaemias and prostate cancers. Sequences of the invention  
are used as vaccines and in gene therapy. The present sequence is human  
calreticulin protein.

Sequence 417 AA:

Query Match 100.0%; Score 60; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;





KW CUB functionality; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.

XX OS Rattus norvegicus.

XX FN W09907406-A1.

XX PD 18-FEB-1999.

XX PF 12-AUG-1998; 98WO-GB02430.

XX PR 12-AUG-1997; 97GB-0016998.

XX PA (OYLE-) UNIV LEICESTER.

XX PI Schmaele W;

XX DR WPI: 1999-180404/15.

XX DR N-PSDB; MAX27253.

PT Use of a CClqR binding domain - to modulate complement ubiquitin  
 (CUB) functionality.

XX PS Claim 9; Page 24-25; 31pp; English.

XX This sequence is a C1q and collectin receptor (CC1qR) binding  
 CC domain. The invention relates to the use of a CClqR binding domain in a  
 CC medicament to effect complement ubiquitin (CUB) functionality, and an  
 CC inhibitor of the CClqR binding domain in a medicament to inhibit CUB  
 CC functionality. The CClqR binding domain, or its inhibitor, can be used to  
 CC treat a human or animal body. Particularly an inhibitor is used to treat  
 CC complement activation involved in the initiation and maintenance of  
 CC inflammation, for example in myocardial infarction, brain ischaemia  
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
 CC plaques in Alzheimer's disease. The use of CClqR binding domain or  
 CC inhibitor enables the CUB domain functionality to be modulated using a  
 CC low molecular weight molecule.

XX SQ Sequence 122 AA;

Query Match 60.0%; Score 36; DB 20; Length 122;

Best Local Similarity 100.0%; Pred. No. 5e-34;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 RCKDDEFTHTLTYLIVRPDNTYEVRKIDNSQVSGSLE 60

DB 1 RCKDDEFTHTLTYLIVRPDNTYEVRKIDNSQVSGSLE 36

Search completed: March 14, 2003, 20:44:19  
 Job time : 10.2006 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 2.38682 Seconds  
(without alignments)  
946.243 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49

Sequence: 1 NYKGNVLIINKDIRCKDDEF.....PDNTYEKIDNSQVSGSLE 49

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEM\_PUB pep:.\*  
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9: /cgn2\_6/ptodata/2/pubppaa/US09\_NEM\_PUB pep:.\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB pep:.\*  
11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEM\_PUB pep:.\*  
12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB pep:.\*  
13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEM\_PUB pep:.\*  
14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB pep:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	417	9 US-09-906-393A-36	Sequence 36, Appl
2	12	24.5	12	9 US-09-906-393A-6	Sequence 6, Appl
3	6	12.2	116	9 US-10-078-770-128	Sequence 128, App
4	6	12.2	125	9 US-10-078-770-132	Sequence 132, App
5	6	12.2	218	9 US-09-925-664-14	Sequence 14, Appl
6	6	12.2	218	10 US-09-189-833B-7	Sequence 7, Appl
7	6	12.2	218	10 US-09-189-833B-8	Sequence 8, Appl
8	6	12.2	218	10 US-09-902-705-7	Sequence 7, Appl
9	6	12.2	218	10 US-09-902-705-8	Sequence 8, Appl
10	6	12.2	226	9 US-09-895-913A-362	Sequence 362, App
11	6	12.2	247	10 US-09-815-242-11342	Sequence 11342, A
12	6	12.2	247	10 US-09-815-242-11514	Sequence 11514, A
13	6	12.2	250	12 US-10-062-254-90	Sequence 90, Appl
14	6	12.2	289	10 US-09-815-242-14056	Sequence 14056, A
15	6	12.2	295	10 US-09-815-242-11836	Sequence 11836, A
16	6	12.2	312	9 US-09-966-459A-10	Sequence 10, Appl
17	6	12.2	318	10 US-09-761-569-2	Sequence 2, Appl
18	6	12.2	351	10 US-09-796-033-6	Sequence 6, Appl
19	6	12.2	351	10 US-09-730-465-6	Sequence 6, Appl

20	6	12.2	411	9 US-10-002-050-10	Sequence 10, Appl
21	6	12.2	411	9 US-10-002-304-10	Sequence 10, Appl
22	6	12.2	411	12 US-10-003-152-10	Sequence 150, Appl
23	6	12.2	423	10 US-09-729-674-160	Sequence 160, App
24	6	12.2	434	10 US-09-430-221-4	Sequence 4, Appl
25	6	12.2	464	9 US-10-002-050-20	Sequence 20, Appl
26	6	12.2	464	12 US-10-002-304-20	Sequence 20, Appl
27	6	12.2	464	12 US-10-003-152-20	Sequence 20, Appl
28	6	12.2	469	10 US-09-815-242-11533	Sequence 11533, A
29	6	12.2	537	9 US-09-738-626-6798	Sequence 6798, Ap
30	6	12.2	537	9 US-09-738-626-4471	Sequence 4471, Ap
31	6	12.2	840	9 US-10-078-770-134	Sequence 134, App
32	6	12.2	948	9 US-09-738-626-6040	Sequence 6040, Ap
33	5	10.2	6	10 US-09-848-353A-3	Sequence 3, Appl
34	5	10.2	6	10 US-08-868-353A-7	Sequence 7, Appl
35	5	10.2	9	10 US-09-966-264-14	Sequence 14, Appl
36	5	10.2	13	10 US-09-950-313-52	Sequence 52, Appl
37	5	10.2	15	10 US-09-925-442-21	Sequence 21, Appl
38	5	10.2	15	10 US-09-925-442-22	Sequence 22, Appl
39	5	10.2	27	9 US-09-974-879-357	Sequence 357, App
40	5	10.2	33	9 US-10-081-816-84	Sequence 84, Appl
41	5	10.2	38	10 US-09-729-674-26	Sequence 26, Appl
42	5	10.2	40	10 US-09-864-761-42048	Sequence 42048, A
43	5	10.2	41	10 US-09-867-852-75	Sequence 75, Appl
44	5	10.2	43	10 US-09-925-300-1050	Sequence 1050, Ap
45	5	10.2	49	10 US-09-864-761-36566	Sequence 36566, A

## ALIGNMENTS

RESULT 1  
US-09-906-393A-36  
; Sequence 36, Application US/09906393A  
; Publication No. US20030039970A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906,393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-906-393A-36

Query Match 100.0%; Score 49; DB 9; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.6e-43;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLIINKDIRCKDDEFTHLYTLVPPDNTYEKIDNSQVSGSLE 49  
Db 149 NYKGNVLIINKDIRCKDDEFTHLYTLVPPDNTYEKIDNSQVSGSLE 197

RESULT 2  
US-09-906-393A-6  
; Sequence 6, Application US/09906393A  
; Publication No. US20030039970A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906,393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761

;; PRIOR FILING DATE: 2000-07-17  
;; NUMBER OF SEQ ID NOS: 36  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 6  
;; LENGTH: 12  
;; TYPE: PRT  
;; ORGANISM: homo sapiens  
US-09-906-393A-6

Query Match 24.5%; Score 12; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 INKDIRCKDDEF 20  
DB 1 INKDIRCKDDEF 12

RESULT 3  
US-10-078-770-128  
;; Sequence 128, Application US/10078770  
;; Publication No. US20030003471A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Famodu, Omolayo O.  
;; APPLICANT: Forge, Charlie  
;; APPLICANT: Miao, Guo-Hua  
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides  
;; FILE REFERENCE: BB-1365 US NA  
;; CURRENT APPLICATION NUMBER: US/10/078,770  
;; PRIOR FILING DATE: 2002-02-19  
;; PRIOR APPLICATION NUMBER: 09/614,188  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,400  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/153,534  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: 60/161,223  
;; PRIOR FILING DATE: 1999-10-22  
;; PRIOR APPLICATION NUMBER: 60/159,878  
;; PRIOR FILING DATE: 1999-10-15  
;; PRIOR APPLICATION NUMBER: 60/157,401  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/143,419  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,409  
;; PRIOR FILING DATE: 1999-07-12  
;; NUMBER OF SEQ ID NOS: 196  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 128  
;; LENGTH: 116  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: UNSURE  
;; LOCATION: (92)..(93)  
;; NAME/KEY: UNSURE  
;; LOCATION: (98)  
;; NAME/KEY: UNSURE  
;; LOCATION: (100)  
US-10-078-770-128

Query Match 12.2%; Score 6; DB 9; Length 116;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9  
DB 26 GKNVLI 31

RESULT 4  
US-10-078-770-132  
;; Sequence 132, Application US/10078770

;; Publication No. US20030003471A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Famodu, Omolayo O.  
;; APPLICANT: Forge, Charlie  
;; APPLICANT: Miao, Guo-Hua  
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides  
;; FILE REFERENCE: BB-1365 US NA  
;; CURRENT APPLICATION NUMBER: US/10/078,770  
;; CURRENT FILING DATE: 2002-02-19  
;; PRIOR APPLICATION NUMBER: 09/614,188  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,400  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/153,534  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: 60/161,223  
;; PRIOR FILING DATE: 1999-10-22  
;; PRIOR APPLICATION NUMBER: 60/159,878  
;; PRIOR FILING DATE: 1999-10-15  
;; PRIOR APPLICATION NUMBER: 60/157,401  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/143,419  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,409  
;; PRIOR FILING DATE: 1999-07-12  
;; NUMBER OF SEQ ID NOS: 196  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 132  
;; LENGTH: 125  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
US-10-078-770-132

Query Match 12.2%; Score 6; DB 9; Length 125;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9  
DB 33 GKNVLI 38

RESULT 5  
US-09-925-664-14  
;; Sequence 14, Application US/09925664  
;; Patent No. US2002016006A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Denney, Jr., Dan W.  
;; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia  
;; FILE REFERENCE: GENITOPE-06499  
;; CURRENT APPLICATION NUMBER: US/09/925,664  
;; CURRENT FILING DATE: 2001-08-09  
;; PRIOR APPLICATION NUMBER: 09/370,453  
;; PRIOR FILING DATE: 1999-08-09  
;; PRIOR APPLICATION NUMBER: 08/644,664  
;; PRIOR FILING DATE: 1996-05-01  
;; PRIOR APPLICATION NUMBER: 08/761,277  
;; PRIOR FILING DATE: 1996-12-06  
;; NUMBER OF SEQ ID NOS: 80  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 14  
;; LENGTH: 218  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-925-664-14

Query Match 12.2%; Score 6; DB 9; Length 218;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9  
DB 127 GKNVLI 132

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RESULT 6
US-09-189-833B-7
; Sequence 7, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-7

Query Match          12.2%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
      |||||
DB 127 GKNVLI 132

RESULT 7
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match          12.2%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
      |||||
DB 127 GKNVLI 132

RESULT 8
US-09-902-705-7
; Sequence 7, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
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; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-7

Query Match          12.2%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
      |||||
DB 127 GKNVLI 132

RESULT 9
US-09-902-705-8
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

Query Match          12.2%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
      |||||
DB 127 GKNVLI 132

RESULT 10
US-09-895-913A-362
; Sequence 362, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 362
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 224
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-913A-362

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Query Match      12.2% Score 6; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 GKNVLI 9
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DB 5 GKNVLI 10

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RESULT 11

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US-09-815-242-11342
; Sequence 11342, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

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; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11342
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11342

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Query Match      12.2% Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 GKNVLI 9
    |||||
DB 5 GKNVLI 10

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RESULT 12

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US-09-815-242-11514
; Sequence 11514, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

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```

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

```

```

; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11514
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11514

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Query Match      12.2% Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 GKNVLI 9
    |||||
DB 5 GKNVLI 10

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RESULT 13

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US-10-062-254-90
; Sequence 90, Application US/10062254
; Patent No. US2002013882A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Cahoon, Edgar B
; APPLICANT: Falco, Rebecca E
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Rua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun

```

```

; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006

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;; PRIOR FILING DATE: 1999-09-23  
;; PRIOR APPLICATION NUMBER: 60/156899  
;; PRIOR FILING DATE: 1999-09-30  
;; PRIOR APPLICATION NUMBER: 60/157287  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/169767  
;; PRIOR FILING DATE: 1999-12-09  
;; PRIOR APPLICATION NUMBER: 60/171054  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: 60/172958  
;; PRIOR FILING DATE: 1999-12-21  
;; PRIOR APPLICATION NUMBER: 60/171515  
;; PRIOR FILING DATE: 1999-12-22  
;; PRIOR APPLICATION NUMBER: 60/173535  
;; PRIOR FILING DATE: 1999-12-29  
;; NUMBER OF SEQ ID NOS: 375  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 90  
;; LENGTH: 250  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
US-10-062-254-90

Query Match 12.2%; Score 6; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 QVSSGS 47  
Db 28 QVSSGS 33

RESULT 14

US-09-815-242-14056  
; Sequence 14056, Application US/09815242  
; Patent NO. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14056  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Salmonella typhi  
US-09-815-242-14056

Query Match 12.2%; Score 6; DB 10; Length 289;

Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLINKD 12  
Db 3 VLINKD 8

RESULT 15

US-09-815-242-11836  
; Sequence 11836, Application US/09815242  
; Patent NO. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11836  
; LENGTH: 295  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-11836

Query Match 12.2%; Score 6; DB 10; Length 295;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLINKD 12  
Db 3 VLINKD 8

Search completed: March 14, 2003, 20:51:11  
Job time : 3.38682 secs





GenCore version 5.1.4.P5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 2.76122 Seconds  
(Without alignments)  
522.132 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49  
Sequence: 1 NYGKNVLIKIDRCKDDEF.....PDNTYEKIDNSQVESGSL 49

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued\_patents\_AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Length	ID	Description
1	7	14.3	593	1 US-08-296-362-2	Sequence 2, Appl
2	6	12.2	69	4 US-09-134-001C-5362	Sequence 5362, Ap
3	6	12.2	74	4 US-09-134-001C-4815	Sequence 4815, Ap
4	6	12.2	94	4 US-09-134-001C-5410	Sequence 5410, Ap
5	6	12.2	184	3 US-08-630-172-2	Sequence 2, Appl
6	6	12.2	184	4 US-09-375-419-2	Sequence 2, Appl
7	6	12.2	185	4 US-09-384-162-11	Sequence 11, Appl
8	6	12.2	218	1 US-08-644-664B-14	Sequence 14, Appl
9	6	12.2	218	1 US-08-761-277A-14	Sequence 14, Appl
10	6	12.2	318	1 US-08-530-850-2	Sequence 2, Appl
11	6	12.2	318	1 US-08-446-083-2	Sequence 2, Appl
12	6	12.2	318	4 US-08-888-429A-2	Sequence 2, Appl
13	6	12.2	318	4 US-09-149-879-2	Sequence 2, Appl
14	6	12.2	351	4 US-08-466-465-6	Sequence 6, Appl
15	6	12.2	418	3 US-08-630-172-18	Sequence 18, Appl
16	6	12.2	418	4 US-09-375-419-18	Sequence 18, Appl
17	6	12.2	504	4 US-09-499-302A-6	Sequence 6, Appl
18	6	12.2	512	2 US-08-557-122A-33	Sequence 33, Appl
19	6	12.2	512	2 US-09-262-666-33	Sequence 33, Appl
20	6	12.2	812	1 US-08-446-794A-4	Sequence 4, Appl
21	6	12.2	891	4 US-09-134-001C-4913	Sequence 4913, Ap
22	5	10.2	6	4 US-08-874-197-3	Sequence 3, Appl
23	5	10.2	6	4 US-08-874-197-7	Sequence 7, Appl
24	5	10.2	6	4 US-08-648-182-3	Sequence 3, Appl
25	5	10.2	6	4 US-08-648-182-7	Sequence 7, Appl
26	5	10.2	10	1 US-08-594-447-12	Sequence 12, Appl
27	5	10.2	10	1 US-08-541-964-11	Sequence 11, Appl

28	5	10.2	10	2 US-08-665-647-26	Sequence 26, Appl
29	5	10.2	12	1 US-08-446-856A-10	Sequence 10, Appl
30	5	10.2	12	1 US-08-446-856A-11	Sequence 11, Appl
31	5	10.2	15	1 US-08-447-411-64	Sequence 64, Appl
32	5	10.2	15	2 US-08-662-227-21	Sequence 21, Appl
33	5	10.2	15	2 US-08-662-227-22	Sequence 22, Appl
34	5	10.2	15	4 US-09-017-947-21	Sequence 21, Appl
35	5	10.2	15	4 US-09-017-947-22	Sequence 22, Appl
36	5	10.2	20	3 US-08-467-023-38	Sequence 38, Appl
37	5	10.2	20	3 US-08-467-023-39	Sequence 39, Appl
38	5	10.2	22	3 US-09-024-020B-18	Sequence 18, Appl
39	5	10.2	22	4 US-09-425-043-18	Sequence 18, Appl
40	5	10.2	36	1 US-08-190-802A-133	Sequence 133, Appl
41	5	10.2	36	1 US-08-190-802A-177	Sequence 177, Appl
42	5	10.2	36	4 US-08-477-346-133	Sequence 133, Appl
43	5	10.2	36	4 US-08-477-346-177	Sequence 177, Appl
44	5	10.2	36	4 US-08-473-089-133	Sequence 133, Appl
45	5	10.2	36	4 US-08-473-089-177	Sequence 177, Appl

## ALIGNMENTS

RESULT 1  
US-08-296-362-2  
; Sequence 2, Application US/08296362  
; Patent No. 5691306  
; GENERAL INFORMATION:  
; APPLICANT: Bergeron, John J.M.  
; APPLICANT: Thomas, David Y.  
; APPLICANT: Mada, Ikko  
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF  
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY  
; TITLE OF INVENTION: PROTEIN PRODUCTION  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/296,362  
; FILING DATE: 25-AUG-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deehr, Manya S.  
; REGISTRATION NUMBER: 37,120  
; REFERENCE/DOCKET NUMBER: 690066.401C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 593 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-296-362-2  
Query Match 14.3%; Score 7%; DB 1;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 21 THLTLLI 27  
|||||||

Db 236 HLYTLI 242

RESULT 2

US-09-134-001C-5362  
; Sequence 5362, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5362  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5362

Query Match

12.2%; Score 6; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 NVLINK 11

Db 29 NVLINK 34

RESULT 3

US-09-134-001C-4815  
; Sequence 4815, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4815  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4815

Query Match

12.2%; Score 6; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 HLYTLI 27

Db 15 HLYTLI 20

RESULT 4

US-09-134-001C-5410  
; Sequence 5410, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 5410  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5410

Query Match

12.2%; Score 6; DB 4; Length 94;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 NVLINK 11

Db 21 NVLINK 26

RESULT 5

US-08-630-172-2  
; Sequence 2, Application US/08630172  
; Patent No. 6060054  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,172  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2879-36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 184 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-630-172-2

Query Match

12.2%; Score 6; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 KGNVL 8

Db 89 KGNVL 94

RESULT 6

US-09-375-419-2  
; Sequence 2, Application US/09375419  
; Patent No. 6264950  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/375,419  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/630,172  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2879-36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 184 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-375-419-2  
Query Match 12.2%; Score 6; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 3 GKNVL 8  
Db 89 GKNVL 94  
RESULT 7  
US-09-384-162-11  
; Sequence 11, Application US/09384162  
; Patent No. 6376747  
; GENERAL INFORMATION:  
; APPLICANT: Xing, Ti  
; APPLICANT: Malik, Kamal  
; APPLICANT: Martin-Heller, Teresa  
; APPLICANT: Miki L., Brian  
; TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase  
; FILE REFERENCE: 08-884280US  
; CURRENT APPLICATION NUMBER: US/09/384,162  
; CURRENT FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-384-162-11  
Query Match 12.2%; Score 6; DB 4; Length 185;

Best Local Similarity 100.0%; Pred. No. 38;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 NVLNLK 11  
Db 108 NVLNLK 113  
RESULT 8  
US-08-644-664B-14  
; Sequence 14, Application US/08644664B  
; Patent No. 5776746  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Gene Amplification Methods  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/644,664B  
; FILING DATE: 01-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: GENITOP-00912  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-644-664B-14  
Query Match 12.2%; Score 6; DB 1; Length 218;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 GKNVLI 9  
Db 127 GKNVLI 132  
RESULT 9  
US-08-761-277A-14  
; Sequence 14, Application US/08761277A  
; Patent No. 5972334  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,277A  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/644,664  
FILING DATE: 01-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamlin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: GENITOPPE-02406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-761-277A-14

Query Match 12.2%; Score 6; DB 2; Length 218;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GRNVL1 9  
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Db 127 GRNVL1 132

RESULT 10  
US-08-530-950-2  
Sequence 2, Application US/08530950  
GENERAL INFORMATION:  
PATENT No. 5736381  
APPLICANT: Davis, Roger J.  
APPLICANT: Ringeaud, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Derjard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/530,950  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
US-08-530-950-2

Query Match 12.2%; Score 6; DB 1; Length 318;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVLINK 11  
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Db 166 NVLINK 171

RESULT 11  
US-08-446-083-2  
Sequence 2, Application US/08446083  
PATENT No. 5804427  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Ringeaud, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Derjard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,083  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 04020/066001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-446-083-2

Query Match 12.2%; Score 6; DB 1; Length 318;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVLINK 11  
|||||  
Db 166 NVLINK 171

RESULT 12  
US-08-888-429A-2

Sequence 2, Application US/08888429A  
Patent No. 6136596  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Whitmarsh, Alan  
APPLICANT: Tournier, Cathy  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, Peter J.  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 299354  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-888-429A-2

Query Match 12.2%; Score 6; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVLINK 11  
Db 166 NVLINK 171

RESULT 13  
US-09-149-879-2  
Sequence 2, Application US/09149879  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Rahngaund, Joeli  
APPLICANT: Gupta, Shashi  
APPLICANT: Derijard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/149,879  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200134  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
US-09-149-879-2

Query Match 12.2%; Score 6; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVLINK 11  
Db 166 NVLINK 171

RESULT 14  
US-08-466-465-6  
Sequence 6, Application US/08466465  
Patent No. 6162432  
GENERAL INFORMATION:  
APPLICANT: Wallner, Barbara P.  
APPLICANT: Cooper, Kevin D.  
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen  
TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using  
TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,465  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/08755  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/862,022  
FILING DATE: 12-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/770,969

Search completed: March 14, 2003, 20:50:09  
Job time : 3.76122 secs

FILING DATE: 07-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis (PLM)  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: BGP-111CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-466-465-6

Query Match 12.2%; Score 6; DB 4; Length 351;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KGNVL 8  
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Db 113 KGNVL 118

RESULT 15  
US-08-630-172-18  
Sequence 18, Application US/08630172  
Patent No. 6060054  
GENERAL INFORMATION:  
APPLICANT: Staertz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
TITLE OF INVENTION: LYMPHOCYTE VETO  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 418 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-18

Query Match 12.2%; Score 6; DB 3; Length 418;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KGNVL 8  
|||||  
Db 89 KGNVL 94

GenCore version 5.1.4-p5.4578  
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## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 30.6017 Seconds

(Without alignments)  
783.783 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180  
Sequence: 1 EPAVYFKEDGFLDCDGMTSRM.....PDNTVEYKIDNSQVESGSLE 180

## Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

## Database :

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21: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	180	100.0	180	21	AAV92351	Human vasostatin (
2	180	100.0	400	21	AAV92350	Recombinant human
3	180	100.0	417	10	AAV92276	60 kD Ro (Ro/SSA)
4	180	100.0	417	21	AAV92349	Human MBP-calretic
5	180	100.0	417	23	AAV924591	Human calreticulin
6	180	100.0	417	23	AAU77712	Human calreticulin
7	180	100.0	417	23	AAE18851	Human calreticulin
8	162	90.0	417	20	AAV00927	Human calreticulin
9	96	53.3	177	23	ABP42414	Human ovarian anti
10	77	42.8	401	18	AAW11156	Calreticulin. Hom

11	61	33.9	61	21	AAV92352	Recombinant human
12	60	33.3	60	21	AAV92354	Recombinant human
13	60	33.3	280	21	AAV92355	Recombinant delta-
14	49	27.2	49	21	AAV92353	Recombinant human
15	36	20.0	122	20	AAV00924	Human cC1qR bindin
16	36	20.0	122	20	AAV00926	Rat cC1qR binding
17	19	10.6	122	20	AAV00925	Mouse cC1qR bindin
18	19	10.6	336	12	AAV12312	Partial sequence o
19	19	10.6	406	22	ABR64414	Drosophila melanog
20	17	9.4	403	17	AAW04171	Flea calreticulin
21	15	8.3	15	19	AAW76256	Human calreticulin
22	14	7.8	14	19	AAW76270	Human calreticulin
23	14	7.8	15	18	AAW7317	Alpha-human fructo
24	14	7.8	15	20	AAV02460	Fragment of human
25	12	6.7	12	19	AAW76267	Human calreticulin
26	12	6.7	12	19	AAW76268	Human calreticulin
27	12	6.7	12	23	AAE18840	Human calreticulin
28	11	6.1	11	19	AAW76266	Human calreticulin
29	11	6.1	11	19	AAW76269	Human calreticulin
30	10	5.6	11	23	AAE18839	Human calreticulin
31	9	5.0	9	19	AAW76265	Human calreticulin
32	9	5.0	84	21	AAV41018	Zea mays protein f
33	9	5.0	312	21	AAV424609	Arabidopsis thalia
34	9	5.0	312	21	AAV47933	Arabidopsis thalia
35	9	5.0	332	21	AAV30998	Arabidopsis thalia
36	9	5.0	385	21	AAV32385	Human secreted pro
37	9	5.0	415	22	AAV66341	Castor bean calret
38	9	5.0	415	22	AAV66343	Castor bean calret
39	9	5.0	420	23	ABR04656	Maize calreticulin
40	9	5.0	421	21	AAV24608	Arabidopsis thalia
41	9	5.0	421	21	AAV47932	Arabidopsis thalia
42	9	5.0	424	21	AAV24607	Arabidopsis thalia
43	9	5.0	424	21	AAV47931	Arabidopsis thalia
44	9	5.0	441	21	AAV30997	Arabidopsis thalia
45	9	5.0	444	21	AAV30996	Arabidopsis thalia

## ALIGNMENTS

RESULT 1	
AAV92351	AAV92351 standard; Protein; 180 AA.
XX	XX
AC	AAV92351;
DT	10-AUG-2000 (first entry)
XX	XX
XX	Human vasostatin (calreticulin N-terminal 180 amino acids).
XX	MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
KW	angiogenesis; inhibition; endothelial cell; anti-angiogenic;
KW	neuroprotective; antidiabetic; cytosolic; dermatological; hepatic;
KW	immunosuppressive; anti-inflammatory; anti-atherosclerotic;
KW	gastrointestinal; anti-arthritis; ophthalmic.
XX	XX
OS	Homo sapiens.
XX	Synthetic.
XX	XX
PN	W0200020577-A1.
XX	XX
PD	13-APR-2000.
XX	XX
PF	05-OCT-1999; 99W0-US23240.
XX	XX
PR	06-OCT-1998; 98US-0103438.
XX	XX
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	XX
PI	Tosato G, Pike SE, Yao L;
XX	XX
DR	WPI; 2000-303767/26.
XX	XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 PS Claim 4; Page 82; 99pp; English.  
 XX  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 CC  
 SQ Sequence 180 AA;  
 Query Match 100.0%; Score 180; DB 21; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-187;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKFLVSSGKFGDEEKDKGLQTSQDARFYAL 60  
 DB 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKFLVSSGKFGDEEKDKGLQTSQDARFYAL 60  
 QY 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEVYIMFGPDIC 120  
 DB 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEVYIMFGPDIC 120  
 QY 121 GGGTTRKVVHVFYFKGKNVLIINKDIRCKDEFTLTLVLRPNTEYEVKIDNSQVSGSLE 180  
 DB 121 GGGTTRKVVHVFYFKGKNVLIINKDIRCKDEFTLTLVLRPNTEYEVKIDNSQVSGSLE 180  
 RESULT 2  
 AAY92350  
 ID AAY92350 standard; Protein; 400 AA.  
 AC AAY92350;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant human MBP-calreticulin.  
 XX  
 KM MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KM cyostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
 KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000020577-A1.  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI: 2000-303767/26.  
 DR N-PSDB: AAA09346; AAA09347.  
 XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 PS Claim 4; Page 80-81; 99pp; English.  
 XX  
 CC Recombinant human MBP-calreticulin comprises the sequence of human  
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 CC  
 SQ Sequence 400 AA;  
 Query Match 100.0%; Score 180; DB 21; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-187;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKFLVSSGKFGDEEKDKGLQTSQDARFYAL 60  
 DB 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKFLVSSGKFGDEEKDKGLQTSQDARFYAL 60  
 QY 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEVYIMFGPDIC 120  
 DB 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEVYIMFGPDIC 120  
 QY 121 GGGTTRKVVHVFYFKGKNVLIINKDIRCKDEFTLTLVLRPNTEYEVKIDNSQVSGSLE 180  
 DB 121 GGGTTRKVVHVFYFKGKNVLIINKDIRCKDEFTLTLVLRPNTEYEVKIDNSQVSGSLE 180  
 RESULT 3  
 AAP92276  
 ID AAP92276 standard; protein; 417 AA.  
 AC AAP92276;  
 XX  
 DT 23-FEB-1990 (first entry)  
 XX  
 DE 60 kD Ro (Ro/SSA) antigen.  
 XX  
 KM Sjorens syndrome; systemic lupus erythematosus.  
 KM Synthetic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO8909273-A.  
 PD 05-OCT-1989.  
 XX  
 PF 22-MAR-1989; 89WO-US01213.  
 XX  
 PR 22-MAR-1988; 88US-0171634.  
 XX  
 PA (TEXA ) UNIV OF TEXAS SYST.  
 XX  
 PI Sontheimer RD, Capra JD, McCaulliffe DP;  
 XX  
 DR WPI: 1989-309537/42.  
 DR N-PSDB: AAP92276.  
 XX  
 PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen



PT - used in immunoassays to detect rheumatic disease  
XX  
PS Disclosure; Fig 2; 88pp; English.  
XX  
CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
CC expressed recombinantly to detect autoantibodies, for identification  
CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,  
CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
CC antigens.  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 180; DB 10; Length 417;  
Best Local Similarity 100.0%; Pred. No. 9,8e-187;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPAYVFKQFLDGDGWTSMIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60  
DB 18 EPAYVFKQFLDGDGWTSMIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 77  
QY 61 SASPEFSNKGOTLVQFTVKHEQINDCGGCVKLFPPNSLDQTDHGDSEYIMFGPDIC 120  
DB 78 SASPEFSNKGOTLVQFTVKHEQINDCGGCVKLFPPNSLDQTDHGDSEYIMFGPDIC 137  
QY 121 GPGTKKVVHVFNYKGNVLLINKDIRCKDEFTHTLTVLRPNTYEVKIDNSQVSSGLE 180  
DB 138 GPGTKKVVHVFNYKGNVLLINKDIRCKDEFTHTLTVLRPNTYEVKIDNSQVSSGLE 197  
RESULT 4  
ID AAY92349 standard; Protein: 417 AA.  
XX  
AC AAY92349;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Human MBP-calreticulin.  
XX  
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; anti-diabetic;  
KW cytoskeletal; dermatological; immunosuppressive; anti-inflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..17  
FT /label= signal\_peptide  
FT Protein 18  
FT /label= mature\_protein  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US23240.  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Tosato G, Pike SE, Yao L;  
XX  
DR WPI; 2000-303767/26.  
XX  
DR N-PSDB; AAA09346, AAA09347.  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
PS Disclosure; Page 79-80; 99pp; English.  
XX  
CC A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trichoma, neovascular glaucoma, psoriasis, angiodermas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 180; DB 21; Length 417;  
Best Local Similarity 100.0%; Pred. No. 9,8e-187;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 18 EPAYVFKQFLDGDGWTSMIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 77  
QY 61 SASPEFSNKGOTLVQFTVKHEQINDCGGCVKLFPPNSLDQTDHGDSEYIMFGPDIC 120  
DB 78 SASPEFSNKGOTLVQFTVKHEQINDCGGCVKLFPPNSLDQTDHGDSEYIMFGPDIC 137  
QY 121 GPGTKKVVHVFNYKGNVLLINKDIRCKDEFTHTLTVLRPNTYEVKIDNSQVSSGLE 180  
DB 138 GPGTKKVVHVFNYKGNVLLINKDIRCKDEFTHTLTVLRPNTYEVKIDNSQVSSGLE 197  
RESULT 5  
ID AAE24591 standard; Protein: 417 AA.  
XX  
AC AAE24591;  
XX  
DT 04-OCT-2002 (first entry)  
XX  
DE Human calreticulin protein.  
XX  
KW Human; calreticulin; antisense compound; hyperproliferative disorder;  
KW cancer; autoimmune disease; viral infection; cardiovascular disease;  
KW antisense therapy; cytostatic; immunosuppressive; virucide.  
XX  
OS Homo sapiens.  
XX  
PN WO200236743-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 30-OCT-2001; 2001WO-US49045.  
XX  
PR 30-OCT-2000; 2000US-0702327.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Cowsett LM;  
XX  
DR WPI; 2002-479759/51.  
XX  
DR N-PSDB; AAD39469.  
XX  
PT Novel antisense compound targeted to nucleic acid encoding  
PT calreticulin, useful for treating a human having disease or condition  
PT associated with calreticulin e.g. cancer, viral infection, autoimmune  
PT disease -  
XX  
PS Disclosure; Page 88-90; 109pp; English.  
XX

CC The invention relates to antisense compounds, compositions and methods  
CC for modulating the expression of calreticulin. The compositions comprise  
CC antisense compounds, particularly antisense oligonucleotides, targeted  
CC to nucleic acids encoding calreticulin. The antisense compound is useful  
CC for inhibiting the expression of calreticulin in human cells or tissues.  
CC It is also useful for treating a human having a disease or condition  
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.,  
CC cancer, autoimmune disease, viral infection or cardiovascular disease,  
CC by inhibiting expression of calreticulin. It is useful for diagnostics,  
CC therapeutics, prophylaxis and as research reagents and kits. It is also  
CC used in antisense therapy. The present sequence is human calreticulin  
CC protein. This sequence is used in the exemplification of the invention.

XX Sequence 417 AA:

Query Match 100.0%; Score 180; DB 23; Length 417;

Best Local Similarity 100.0%; Pred. No. 9.8e-187;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKDFLDGDTSMWIESKHSDFGKFLVSSGKRYGDEKDKGLQTSODARFVAL 60  
DB 18 EPAVYFKDFLDGDTSMWIESKHSDFGKFLVSSGKRYGDEKDKGLQTSODARFVAL 77  
QY 61 SASFEFSSKGGTLLVQFTVKHEQNDICGGGYVKLEPNSLDQTDHMGDSEYNIMEGPDIC 120  
DB 78 SASFEFSSKGGTLLVQFTVKHEQNDICGGGYVKLEPNSLDQTDHMGDSEYNIMEGPDIC 137  
QY 121 GEGTKKVHVYIFNFKGNVLIINKDIRCKDDEFTHLYTLIYRPDNTYEVKIDNSQVESGSLE 180  
DB 138 GEGTKKVHVYIFNFKGNVLIINKDIRCKDDEFTHLYTLIYRPDNTYEVKIDNSQVESGSLE 197

RESULT 6

AAU77712  
ID AAU77712 standard; Protein; 417 AA.

XX AAU77712;

DT 05-JUN-2002 (first entry)

DE Human calreticulin (CRT).

XX Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;  
KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;  
KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;  
KW tumour; cancer; cervical cancer.

XX Homo sapiens.

OS Homo sapiens.

XX WO200212281-A2.

XX 14-FEB-2002.

PF 02-AUG-2001; 2001WO-US24134.

PR 03-AUG-2000; 2000US-222902P.

PA (UYJO ) UNIV JOHNS HOPKINS.

PI Wu T, Hung C;

DR WPI: 2002-257463/30.

DR N-PSDB; ABR11662.

XX New nucleic acids encoding a fusion polypeptide comprising an  
XX endoplasmic reticulum chaperone polypeptide linked to an antigenic  
XX polypeptide, useful as a vaccine for inducing antigen-specific immune  
XX responses

PS Disclosure; Page 27; 71pp; English.

XX The invention describes a nucleic acid molecule (I) encoding a fusion  
XX polypeptide comprising a first polypeptide domain comprising an

CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and  
CC a second polypeptide domain comprising at least one antigenic peptide  
CC e.g. Human Papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as  
CC a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune  
CC responses, particularly those mediated by cytotoxic T lymphocytes. The  
CC nucleic acid and compositions comprising the nucleic acid is also useful  
CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.  
CC This is the amino acid sequence of the human calreticulin (CRT), an  
CC endoplasmic reticulum protein used in the creation of a DNA vaccine.

XX Sequence 417 AA:

Query Match 100.0%; Score 180; DB 23; Length 417;

Best Local Similarity 100.0%; Pred. No. 9.8e-187;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKDFLDGDTSMWIESKHSDFGKFLVSSGKRYGDEKDKGLQTSODARFVAL 60  
DB 18 EPAVYFKDFLDGDTSMWIESKHSDFGKFLVSSGKRYGDEKDKGLQTSODARFVAL 77  
QY 61 SASFEFSSKGGTLLVQFTVKHEQNDICGGGYVKLEPNSLDQTDHMGDSEYNIMEGPDIC 120  
DB 78 SASFEFSSKGGTLLVQFTVKHEQNDICGGGYVKLEPNSLDQTDHMGDSEYNIMEGPDIC 137  
QY 121 GEGTKKVHVYIFNFKGNVLIINKDIRCKDDEFTHLYTLIYRPDNTYEVKIDNSQVESGSLE 180  
DB 138 GEGTKKVHVYIFNFKGNVLIINKDIRCKDDEFTHLYTLIYRPDNTYEVKIDNSQVESGSLE 197

RESULT 7

AAE18851  
ID AAE18851 standard; Protein; 417 AA.

XX AAE18851;

DT 17-MAY-2002 (first entry)

DE Human calreticulin protein.

XX Human; prostate cancer; calreticulin; T1D-1 protein; TRAITS protein;  
KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;  
KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;  
KW cytosolic; U19 protein.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 98..170

FT Region 98..103

FT Region 149..154

FT Domain 171..285

FT Domain /note="Proline-rich domain (P domain)"

FT Domain /label= C-terminal\_domain

PD 24-JAN-2002.

PF 17-JUL-2001; 2001WO-US22357.

PR 17-JUL-2000; 2000US-218761P.

PR 16-JUL-2001; 2001US-0906393.

PA (NOON ) UNIV NORTHWESTERN.

PI Wang Z, Xiao W;

DR WPI: 2002-179780/23.

DR N-PSDB; AAD29931.

XX Identifying a subject that is likely to have aggressive form of  
PT prostate cancer, involves comparing calreticulin levels in prostate  
PT specimen of the subject and in benign prostatic epithelial cells of the  
PT same subject -  
XX  
XX  
XX  
PS Disclosure: Page 146-148; 148pp; English.  
XX  
CC The present invention relates to methods of distinguishing aggressive  
CC forms of prostate cancer from non-aggressive forms. The method involves  
CC comparing the level of calreticulin in prostate specimen and in benign  
CC prostatic epithelial cells of a subject. The invention particularly  
CC relates to two proteins, namely calreticulin and TR1-1 (TR1A1: 19)  
CC that are down-regulated in aggressive forms of prostate cancer but not  
CC in slowly progressing prostate cancer. They play important roles in  
CC the part of androgen action pathway that suppresses cell proliferation  
CC and/or prevents prostate cancer. The method is useful for identifying  
CC a subject who is likely to have an aggressive form of prostate cancer.  
CC The invention further relates to a method of identifying a subject with  
CC a slow growing form of prostate cancer. TR1-1 sequences are useful for  
CC treating cancers such as epithelium-derived carcinomas, kidney cancers,  
CC lymphomas, leukemias and prostate cancers. Sequences of the invention  
CC are used as vaccines and in gene therapy. The present sequence is human  
CC calreticulin protein.  
XX  
SQ Sequence 417 AA:  
Query Match 100.0%; Score 180; DB 23; Length 417;  
Best Local Similarity 100.0%; Pred. No. 9.8e-187;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 BPAYFKQFLDGDGWTSMIESKHSDEKGFVLSGKRYGDEKDKGLQTSQDAKFYAL 60  
DB 18 BPAYFKQFLDGDGWTSMIESKHSDEKGFVLSGKRYGDEKDKGLQTSQDAKFYAL 77  
QY 61 SASPEFSNKGQTLVVOFTVKHEQNDICGGGYVLFPSNLDQTDHMGDSEYNIMFGPDIC 120  
DB 78 SASPEFSNKGQTLVVOFTVKHEQNDICGGGYVLFPSNLDQTDHMGDSEYNIMFGPDIC 137  
QY 121 GPGTKVHVIVNYKKNVLIKNDIRCKDDEFTHTLTVLRPNTYEKVIDNSQVESGSL 180  
DB 138 GPGTKVHVIVNYKKNVLIKNDIRCKDDEFTHTLTVLRPNTYEKVIDNSQVESGSL 197  
RESULT 8  
AA00927  
ID AA00927 standard; Protein: 417 AA.  
XX  
AC AA00927;  
XX  
XX 28-MAY-1999 (first entry)  
XX  
DE Calreticulin.  
XX  
KW C1g and collectin receptor; cClqR binding domain; complement ubiquitin;  
KW CUB functional; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX PN WO9907406-A1.  
XX  
XX PD 18-FEB-1999.  
XX  
XX PF 12-AUG-1998; 98WO-GB02430.  
XX  
XX PR 12-AUG-1997; 97GB-0016998.  
XX  
XX PA (UYLE-) UNIV LEICESTER.  
XX  
XX PI Schaeble W;

XX  
DR WPI: 1999-180404/15.  
XX  
XX Use of a cClqR binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
PT  
XX  
XX  
PS Disclosure: Page 26-27; 31pp; English.  
XX  
CC This sequence is calreticulin, a homologue of C1q and collectin receptor  
CC (cClqR). The invention relates to the use of a cClqR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
SQ Sequence 417 AA:  
Query Match 90.0%; Score 162; DB 20; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.4e-167;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 19 RMIESKHKDFKGFVLSGKRYGDEKDKGLQTSQDAKFYALSASPEFSNKGQTLVVOF 78  
DB 36 RMIESKHKDFKGFVLSGKRYGDEKDKGLQTSQDAKFYALSASPEFSNKGQTLVVOF 95  
QY 79 TVKHEQNDICGGGYVLFPSNLDQTDHMGDSEYNIMFGPDICGPGTKVHVIVNYKKNV 138  
DB 96 TVKHEQNDICGGGYVLFPSNLDQTDHMGDSEYNIMFGPDICGPGTKVHVIVNYKKNV 155  
QY 139 LINKDIRCKDDEFTHTLTVLRPNTYEKVIDNSQVESGSL 180  
DB 156 LINKDIRCKDDEFTHTLTVLRPNTYEKVIDNSQVESGSL 197  
RESULT 9  
ABP42414  
ID ABP42414 standard; Protein: 177 AA.  
XX  
AC ABP42414;  
XX  
XX 22-AUG-2002 (first entry)  
XX  
DE Human ovarian antigen HOC0062, SEQ ID NO:3546.  
XX  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX PN WO200200677-A1.  
XX  
XX PD 03-JAN-2002.  
XX  
XX PF 07-JUN-2001; 2001WO-US18569.  
XX  
XX PR 07-JUN-2000; 2000US-209467P.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.



PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
PS Claim 4; Page 82-83; 99pp: English.  
XX  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis.  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
CC  
SQ Sequence 61 AA;  
  
Query Match 33.9%; Score 61; DB 21; Length 61;  
Best Local Similarity 100.0%; Pred. No. 2.7e-58;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 120 CGPGRKVVHVFNYKGNVINKDKRCKDEFTHTLTVRPDNTYEKIDNSQVSGSL 179  
Db 1 CGPGRKVVHVFNYKGNVINKDKRCKDEFTHTLTVRPDNTYEKIDNSQVSGSL 60  
QY 180 E 180  
Db 61 E 61  
  
RESULT 12  
AAV92354 standard; Protein: 60 AA.  
XX  
AC AAV92354;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant human calreticulin residues 121-180.  
XX  
KM MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KM cytoskeletal; dermatological; immunosuppressive; antiinflammatory; hepatic;  
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US23240.  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Tosato G, Pike SE, Yao L;  
XX  
DR WPI; 2000-303767/26.  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
PS Claim 4; Page 85; 99pp: English.

XX  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
CC  
SQ Sequence 60 AA;  
  
Query Match 33.3%; Score 60; DB 21; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.2e-57;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 121 GPGTRKVVHVFNYKGNVINKDKRCKDEFTHTLTVRPDNTYEKIDNSQVSGSLE 180  
Db 1 GPGTRKVVHVFNYKGNVINKDKRCKDEFTHTLTVRPDNTYEKIDNSQVSGSLE 60  
  
RESULT 13  
AAV92355 standard; Protein: 280 AA.  
XX  
AC AAV92355;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant delta-120 calreticulin.  
XX  
KM MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KM cytoskeletal; dermatological; immunosuppressive; antiinflammatory; hepatic;  
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US23240.  
XX  
PR 06-OCT-1998; 98US-0103438.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Tosato G, Pike SE, Yao L;  
XX  
DR WPI; 2000-303767/26.  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
PS Claim 4; Page 86; 99pp: English.  
XX  
CC This sequence comprises recombinant human calreticulin (AAV92350)  
CC missing the N-terminal 120 amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The

CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,  
CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
SQ Sequence 280 AA;  
Query Match 33.3%; Score 60; DB 21; Length 280;  
Best Local Similarity 100.0%; Pred. No. 1.3e-56;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 121 GPGTKKVVHYFNKGNVLIINKDIRCKDDEFTHLVTLVPRDNTYEVKIDNSQVESGSL 180  
DB 1 GPGTKKVVHYFNKGNVLIINKDIRCKDDEFTHLVTLVPRDNTYEVKIDNSQVESGSL 60  
RESULT 14  
AAV92353  
ID AAV92353 standard; Protein; 49 AA.  
XX  
AC AAV92353;  
XX  
XX 10-AUG-2000 (first entry)  
DT  
XX  
DE Recombinant human calreticulin residues 132-180.  
XX  
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO20020577-A1.  
PN  
XX  
PD 13-APR-2000.  
XX  
XX 05-OCT-1999; 99WO-0523240.  
PF  
XX  
XX 06-OCT-1998; 98US-0103438.  
PR  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Tosato G, Pike SE, Yao L;  
PI  
XX  
DR WPI: 2000-303767/26.  
XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
XX Claim 4; Page 82-83; 99pp; English.  
PS  
XX  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
SQ Sequence 49 AA;  
Query Match 27.2%; Score 49; DB 21; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.3e-45;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 132 NYGKKNVLIINKDIRCKDDEFTHLVTLVPRDNTYEVKIDNSQVESGSL 180  
DB 1 NYGKKNVLIINKDIRCKDDEFTHLVTLVPRDNTYEVKIDNSQVESGSL 49  
RESULT 15  
AAV00924  
ID AAV00924 standard; Protein; 122 AA.  
XX  
XX AAV00924;  
XX  
XX 28-MAY-1999 (first entry)  
DT  
XX  
XX Human cClqR binding domain protein sequence.  
DE  
XX  
XX C1q and collectin receptor; cClqR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9907406-A1.  
PN  
XX  
XX 18-FEB-1999.  
PD  
XX  
XX 12-AUG-1998; 98WO-GB02430.  
PF  
XX  
XX 12-AUG-1997; 97GB-0016998.  
PR  
XX  
XX (UYLE-) UNIV LEICESTER.  
PA  
XX  
XX Schwaeble W;  
PI  
XX  
XX WPI: 1999-180404/15.  
DR  
XX  
XX N-PSDB; AAX27251.  
DR  
XX  
XX use of a cClqR binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
PT  
XX  
XX Claim 9; Page 23; 31pp; English.  
PS  
XX  
XX This sequence is a C1q and collectin receptor (cClqR) binding  
CC domain. The invention relates to the use of a cClqR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
XX  
SQ Sequence 122 AA;  
Query Match 20.0%; Score 36; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 6.9e-31;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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us-09-807-148-4.oli.ray

Page 9

```
OY      145 RCKDDEFTLTYLIVRPDNTYEKVIDNSQVESGSL 180
          |||||
Db       1   RCKDDEFTHLYTLIVRPDNTYEKVIDNSQVESGSL 36
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Job time : 32.6017 secs

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## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 12.894 Seconds  
(without alignments)  
1342.037 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180  
Sequence: 1 EPAVYFKEDFLDGDGWTSRW.....PDNTYEKIDNSQVESGSLE 180Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR-73:\*  
2: pir1:\*  
3: pir2:\*  
4: pir3:\*  
5: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	100.0	417	1 A37047	calreticulin precu
2	177	42.8	416	1 S06763	calreticulin precu
3	77	42.8	416	1 JH0819	calreticulin precu
4	77	42.8	418	1 A34154	calreticulin precu
5	62	34.4	400	2 S43376	calreticulin, brai
6	62	34.4	421	2 S36799	calreticulin, brai
7	27	15.0	405	1 JH0795	calreticulin precu
8	22	12.2	384	2 S29130	calreticulin (clon
9	22	11.2	411	2 S29129	calreticulin precu
10	20	11.1	419	2 S71343	calreticulin precu
11	19	10.6	336	2 A32507	41K larval antigen
12	19	10.6	406	2 A56637	calreticulin homol
13	14	7.8	29	2 E33208	calreticulin, uter
14	14	7.8	29	2 D33208	calreticulin, brai
15	14	7.8	393	1 A48573	calreticulin, autoa
16	11	6.1	15	2 B33208	calreticulin, uter
17	11	6.1	24	2 A33434	calcium-binding pr
18	11	6.1	29	2 C33208	calreticulin, slow
19	9	5.0	13	2 A33208	calreticulin, hepa
20	9	5.0	15	2 G60977	protein 425 - Cali
21	9	5.0	24	2 A61141	calreticulin, panc
22	9	5.0	389	2 T03691	calreticulin - com
23	9	5.0	395	2 S25851	calreticulin precu
24	9	5.0	412	2 T05703	calreticulin - bar
25	9	5.0	415	2 T10172	calreticulin - dar
26	9	5.0	415	2 T05705	calreticulin - bar
27	9	5.0	416	2 T14554	calreticulin - bee
28	9	5.0	416	2 T16968	calreticulin call
29	9	5.0	421	2 S58170	calreticulin precu

30	9	5.0	422	2 T07841	probable calreticu
31	9	5.0	425	2 C96605	calreticulin (Crt1
32	9	5.0	444	2 H86224	hypothetical prote
33	8	4.4	19	2 S13046	calreticulin - rab
34	8	4.4	574	2 T29137	hypothetical prote
35	7	3.9	93	2 A25343	nonhistone chromos
36	7	3.9	93	2 S05243	histone-like prote
37	7	3.9	178	2 S13717	probable orotate p
38	7	3.9	178	2 D69467	conserved hypotet
39	7	3.9	247	2 H87703	probable choline u
40	7	3.9	305	2 B95943	hypothetical prote
41	7	3.9	313	2 T02534	hypothetical prote
42	7	3.9	358	2 T12850	hypothetical prote
43	7	3.9	359	2 H97254	protein chain rele
44	7	3.9	397	2 C75182	DNA-directed RNA p
45	7	3.9	397	2 G71031	probable DNA-direc

## ALIGNMENTS

RESULT 1  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K Integrin-binding pr  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.  
J. Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
A:Reference number: A42330; MUID:92129342; PMID:1733953  
A:Accession: A42330  
A:Molecule type: DNA  
A:Residues: 1-417 <MC2>  
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
J. Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
A:Reference number: A37047; MUID:90237213; PMID:2332496  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:Cross-references: GB:M3294; NID:g337486; PIDN:AAA36582.1; PID:g337487  
A>Note: the authors translated the codon GTA for residue 349 as Tyr  
R:Kokach, L.A.; Haselby, J.A.; Mellot, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.  
J. Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129; PMID:1919005  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <ROK>  
A:Cross-references: GB:M48739; NID:g179881; PIDN:AAA51916.1; PID:g179882  
A>Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.  
J. Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence  
A:Reference number: A28812; MUID:88273610; PMID:3260607  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LIE>  
A>Note: 18-Ala was also found  
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.  
J. Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
A:Reference number: PH1525; MUID:92115648; PMID:8418194  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DDP>  
A:Experimental source: LAK cell  
R:Roizant, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (C

A:Reference number: A40346; MUID:92002034; PMID:1911778  
 A:Accession: A40346  
 A:Molecule type: protein  
 A:Residues: 18-34; 'R' <ROJ>  
 R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
 Biochem. J. 270, 545-548, 1990  
 A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum retention signal  
 A:Reference number: S11475; MUID:90380058; PMID:2400400  
 A:Accession: S11475  
 A:Molecule type: protein  
 A:Residues: 18-32 <KRA>  
 R:lamerdin, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.  
 submitted to the EMBL Data Library, November 1996  
 A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region  
 A:Reference number: T45075  
 A:Accession: T45075  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-417 <LAMP>  
 A:Cross-references: EMBL:AD000092; PIDN:AA51176.1  
 A:Experimental source: cell line 5HL2-B; fibroblast  
 C:Comment: Antibodies specific for this protein are found in Sjogren's syndrome and in other autoimmune diseases  
 A:Gene: GDB:CALR  
 A:Cross-references: GDB:125179; OMIM:109091  
 A:Map position: 19p13.3-19p13.2  
 A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3  
 A>Note: CRTC  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding; integrin binding  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-417/Product: calreticulin #status predicted <MAT>  
 F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 180; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-103; Indels 0; Gaps 0;  
 Matches 180; Conservative 0; Mismatches 0;

OY 1 EBAVYFEKFDLGGDGTWMSIESKHSKSPGKFEVLSGKFGDEKRGKQTSODARFVAL 60  
 DB 18 EBAVYFEKFDLGGDGTWMSIESKHSKSPGKFEVLSGKFGDEKRGKQTSODARFVAL 77  
 OY 61 SASFEFSKSGQTLVQFVFKHEQNTDGGGYKLEPNSLDQTDHMGDESEYINMEGPDIC 120  
 DB 78 SASFEFSKSGQTLVQFVFKHEQNTDGGGYKLEPNSLDQTDHMGDESEYINMEGPDIC 137  
 OY 121 GGTGKKVHYIYFNKGNVLIINKDIRCKDDEFFHLYTLIYRPDNTYEVKIDNSOVESGSL 180  
 DB 138 GGTGKKVHYIYFNKGNVLIINKDIRCKDDEFFHLYTLIYRPDNTYEVKIDNSOVESGSL 197

RESULT 2  
 S06763  
 calreticulin precursor - mouse  
 N:Alternate names: 55k calcium-binding reticuloplasmic; calregulin  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999  
 C:Accession: S06763; J01444; PC1233; A57498  
 R:Smith, M.J.; Koch, G.L.E.  
 EMBO J. 8, 3581-3586, 1989  
 A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major endoplasmic reticulum protein  
 A:Reference number: S06763; MUID:90059955; PMID:2583110  
 A:Accession: S06763  
 A:Molecule type: DNA  
 A:Residues: 1-416 <SMT>  
 A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568  
 R:Mazatella, R.A.; Gold, P.; Cunningham, M.; Green, M.  
 Gene 120, 217-225, 1992  
 A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calreticulin  
 A:Reference number: J01444; MUID:93013037; PMID:1398135  
 A:Accession: J01444  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <MAZ>

A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085  
 A:Accession: PC1233  
 A:Molecule type: protein  
 A:Residues: 18-41 <MAZ>  
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.  
 J. Biol. Chem. 270, 15926-15929, 1995  
 A:Title: Cell surface calreticulin is a putative mannose-binding lectin which triggers mouse B cell apoptosis  
 A:Reference number: A57498; MUID:95332280; PMID:7608143  
 A:Accession: A57498  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 74-80;142-151;186-193 <WHI>  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-416/Product: calregulin #status experimental <MAT>  
 F:413-416/Region: endoplasmic reticulum retention signal

Query Match 42.8%; Score 77; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-74;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 DMHGDSEYINMEGPDICGFTKRVHYIYFNKGNVLIINKDIRCKDDEFFHLYTLIYRPD 163  
 DB 121 DMHGDSEYINMEGPDICGFTKRVHYIYFNKGNVLIINKDIRCKDDEFFHLYTLIYRPD 180  
 OY 164 TYEVKIDNSOVESGSL 180  
 DB 181 TYEVKIDNSOVESGSL 197

RESULT 3  
 JH0819  
 calreticulin precursor - rat  
 N:Alternate names: calcium-binding protein 3  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text change 20-Jun-2000  
 C:Accession: JH0819; A49176; S11205; PC1109; S45036; S59372; A34473; S13045  
 R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanohe, T.; Arai, K.; Okinaga, E.  
 Exp. Cell Res. 205, 101-110, 1993  
 A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome  
 A:Reference number: A49176; MUID:93202172; PMID:8453984  
 A:Accession: JH0819  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <NAZ>  
 A:Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:g1845572  
 A:Accession: A49176  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-416 <NAZ>  
 A:Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:g1845572  
 A:Experimental source: Sprague-Dawley, spermatogenic cells  
 A>Note: sequence extracted from NCBI backbone (NCBI:127633, NCBI:127643)  
 R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel  
 Nucleic Acids Res. 18, 4933, 1990  
 A:Title: Structural homology between the rat calreticulin gene product and the Onchocerca volvulus protein  
 A:Reference number: S11205; MUID:90370496; PMID:2395661  
 A:Accession: S11205  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <MUR>  
 A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855  
 R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
 A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.  
 A:Reference number: PC1109; MUID:92360010; PMID:1497655  
 A:Accession: PC1109  
 A:Molecule type: protein  
 A:Residues: 18-32 <NAZ>  
 A:Experimental source: testis, strain Sprague-Dawley  
 R:Soenink, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies  
 submitted to the EMBL Data Library, May 1994  
 A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the ER  
 A:Reference number: S45036

A:Accession: S45036  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <SOB>  
A:Cross-references: EMBL:X79327; NID:9488840; PIDN:CAA55890.1; PID:9488841  
R:Lone, Y.C.; Bailey, A.; Lalruffe, N.  
submitted to the EMBL Data Library, December 1988  
A:Reference number: S04867  
A:Accession: S04867  
A:Molecule type: mRNA  
A:Residues: 'R', 270-358, 'AAG' <LON>  
A:Cross-references: EMBL:X13702; NID:956055; PIDN:CAA31987.1; PID:9330260  
A:Note: The authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horinuchi, R.; Kametaki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an  
A:Reference number: S39371; MUID:94072621; PMID:8251535  
A:Accession: S39372  
A:Molecule type: protein  
A:Residues: 18-23, 'X', 25-32 <YOK>  
R:Van, P.N.; Peter, F.; Soelling, H.D.  
J. Biol. Chem. 264, 17494-17501, 1989  
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wi  
lative calcium sequestering rat liver vesicles.  
A:Reference number: A34473; MUID:9008920; PMID:2793869  
A:Accession: A34473  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-36 <VAN>  
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A:Reference number: S13045; MUID:91054414; PMID:2241926  
A:Accession: S13045  
A:Molecule type: protein  
A:Residues: 18-29 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-17/Domain: signal sequence #status predicted <STG>  
F:18-416/Product: calreticulin #status experimental <MAT>  
F:204-212/Region: nuclear location signal  
F:413-416/Region: endoplasmic reticulum retention signal  
F:344/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 42.8%; Score 77; DB 2; Length 416;  
Best Local Similarity 100.0%; Pred. No. 9.1e-74;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 DMHGSEYNIMFGPDICGPTKRVHVFNYKGNVLINKDKCKDEFTHTLTLVLRPN 163  
|||||  
DB 121 DMHGSEYNIMFGPDICGPTKRVHVFNYKGNVLINKDKCKDEFTHTLTLVLRPN 180

OY 164 TYEVKIDNSQVESGSLE 180  
|||||  
DB 181 TYEVKIDNSQVESGSLE 197

RESULT 4  
A34154  
A:Title: calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34154; S13047  
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c  
A:Reference number: A34154; MUID:90094320; PMID:2600080  
A:Accession: A34154  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <FLI>  
A:Cross-references: GB:J05138; NID:9164858; PIDN:AA31188.1; PID:9164859  
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld

Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414; PMID:2241926  
A:Accession: S13047  
A:Molecule type: protein  
A:Residues: 19-32 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: skeletal muscle  
F:1-17/Domain: signal sequence #status predicted <STG>  
F:413-418/Region: endoplasmic reticulum retention signal

Query Match 42.8%; Score 77; DB 1; Length 418;  
Best Local Similarity 100.0%; Pred. No. 9.2e-74;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 DMHGSEYNIMFGPDICGPTKRVHVFNYKGNVLINKDKCKDEFTHTLTLVLRPN 163  
|||||  
DB 121 DMHGSEYNIMFGPDICGPTKRVHVFNYKGNVLINKDKCKDEFTHTLTLVLRPN 180

OY 164 TYEVKIDNSQVESGSLE 180  
|||||  
DB 181 TYEVKIDNSQVESGSLE 197

RESULT 5  
S43376  
A:Title: calreticulin, brain isoform 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
A:Accession: S43376; S36801  
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
Biochem. J. 298, 435-442, 1994  
A:Title: Covalent structure of bovine brain calreticulin.  
A:Reference number: S43376; MUID:94183174; PMID:8135753  
A:Accession: S43376  
A:Molecule type: protein  
A:Residues: 1-400 <MAT>  
A:Experimental source: brain  
R:Lin, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli  
A:Reference number: S36799; MUID:93385184; PMID:8373827  
A:Accession: S36801  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 45-63, 'E', 65-83 <LIU>  
A:Experimental source: brain, clone 8.1  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:397-400/Region: endoplasmic reticulum retention signal  
F:120-146/Disulfide bonds: #status experimental  
F:162/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 34.4%; Score 62; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 8.3e-58;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 LDQTDHMGSEYNIMFGPDICGPTKRVHVFNYKGNVLINKDKCKDEFTHTLTLV 159  
|||||  
DB 100 LDQTDHMGSEYNIMFGPDICGPTKRVHVFNYKGNVLINKDKCKDEFTHTLTLV 159

OY 160 RP 161  
||  
DB 160 RP 161

RESULT 6  
S36799  
A:Title: calreticulin precursor, brain isoform 2 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 13-Aug-1999  
C:Accession: S36799; S36800  
R:Lin, N.; Fine, R.E.; Johnson, R.J.

Biochim. Biophys. Acta 1202, 70-76, 1993  
A>Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.  
A:Reference number: S36799; MUID:93385184; PMID:8373827  
A:Accession: S36799  
A:Molecule type: mRNA  
A:Residues: 1-421 <LTI>  
A:Cross-references: GB:LJ3462; NID:9348693; PIDN:AAC37307.1; PID:9348694  
A:Experimental source: brain, clone 9.4  
A:Accession: S36800  
A:Molecule type: protein  
A:Residues: 35-45 <LTI>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>  
F:418-421/Region: endoplasmic reticulum retention signal  
F:141-167/Disulfide bonds: #status predicted  
F:183/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 34.4%; Score 62; DB 2; Length 421;  
Best Local Similarity 100.0%; Pred. No. 8,7e-58;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 LDQTMHGDSEVIMFGPGICGPTKKVHVITNYKGNVLIKKDIRCKDDETHLYTLIV 159  
|||||  
DB 121 LDQTMHGDSEVIMFGPGICGPTKKVHVITNYKGNVLIKKDIRCKDDETHLYTLIV 180

OY 160 RP 161  
||  
DB 181 RP 182

RESULT 7  
JH0795  
calreticulin precursor - California sea hare

N:Alternate names: protein 407  
C:Species: Aplysia californica (California sea hare)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JH0795; B31409; F60977

R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.  
Neuron 9, 1013-1024, 1992

A>Title: long-term sensitization training in aplysia leads to an increase in calreticulin  
A:Reference number: JH0795; MUID:9309837; PMID:1463604

A:Accession: JH0795  
A:Molecule type: mRNA

A:Residues: 1-405 <KEN>  
A:Cross-references: GB:S51239; NID:9262053; PIDN:AAB24569.1; PID:9262054

A:Experimental source: abdominal ganglion and antral nervous system  
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 89, 7008-7012, 1988

A>Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and  
tion in Aplysia.  
A:Reference number: A94207; MUID:88320566; PMID:3413132

A:Accession: B31409  
A:Molecule type: protein

A:Residues: 'X',17-28,'X',30-31 <KE2>  
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.

Electrophoresis 10, 152-157, 1989  
A>Title: Development of a database of amino acid sequences for proteins identified and  
A:Reference number: A60977; MUID:89276264; PMID:2731514

A:Accession: F60977  
A:Molecule type: protein

A:Residues: 'X',17-28,'X',30-31 <SWE>  
C:Superfamily: calreticulin

C:Keywords: calcium binding; endoplasmic reticulum  
F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-405/Product: calreticulin #status experimental <MAT>  
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 15.0%; Score 27; DB 1; Length 405;  
Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 YNIMFGPDICGPTKKVHVITNYKGN 137  
|||||  
DB 124 YNIMFGPDICGPTKKVHVITNYKGN 150

RESULT 8

S29130  
calreticulin (clone 8) - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29130; T01068

R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992

A>Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997; PMID:1445218

A:Accession: S29130  
A:Molecule type: mRNA

A:Residues: 1-384 <TR>  
A:Cross-references: EMBL:X67598

A:Accession: T01068  
A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-339, 'XTGR' <TR>

A:Cross-references: EMBL:X67598; NID:964610; PIDN:CAA47867.1; PID:964611  
A:Experimental source: CNS

C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:381-384/Region: endoplasmic reticulum retention signal  
F:316/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 12.2%; Score 22; DB 2; Length 384;  
Best Local Similarity 100.0%; Pred. No. 3.1e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 FTHLYTLIVRPDNTYEKIDNS 172  
|||||  
DB 140 FTHLYTLIVRPDNTYEKIDNS 161

RESULT 9

S29129  
calreticulin precursor (clone 3) - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29129

R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992

A>Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997; PMID:1445218

A:Accession: S29129  
A:Molecule type: mRNA

A:Residues: 1-411 <TR>  
A:Cross-references: EMBL:X67597; NID:964608; PIDN:CAA47866.1; PID:964609

A:Experimental source: abdominal ganglion and antral nervous system  
C:Superfamily: calreticulin

C:Keywords: glycoprotein  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-411/Product: calreticulin #status predicted <MAT>

F:408-411/Region: endoplasmic reticulum retention signal  
F:339/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 12.2%; Score 22; DB 2; Length 411;  
Best Local Similarity 100.0%; Pred. No. 3.3e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 FTHLYTLIVRPDNTYEKIDNS 172  
|||||  
DB 163 FTHLYTLIVRPDNTYEKIDNS 184

RESULT 10

S71343  
calreticulin precursor - Korean frog

C:Species: Rana rugosa (Korean frog)

C>Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Jun-2000  
C:Accession: S71343  
R:Yamamoto, S.; Nakamura, M.  
FEBS Lett. 387, 27-32, 1996  
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, *Rana*  
A:Reference number: S71342; MUID:96234004; PMID:8654561  
A:Accession: S71343  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-419 <YAM>  
A:Cross-references: EMBL:D78589; MID:91514956; PIDN:BA11425.1; PID:91514957  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-419/Product: calreticulin #status predicted <MAT>  
F:205-213/Region: nuclear location signal  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 11.1%; Score 20; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 4, 6e-13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HLYTLIVPDMTYEVKIDNS 172  
|||||  
Db 171 HLYTLIVPDMTYEVKIDNS 190

RESULT 11  
A32507  
41K larval antigen - nematode (*Onchocerca volvulus*) (fragment)  
C:Species: *Onchocerca volvulus*  
C>Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 12-Apr-1995  
C:Accession: A32507; A28813  
R:Umasch, T.R.; Gallin, M.T.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.  
J. Clin. Invest. 82, 262-269, 1988  
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of  
A:Reference number: A92769; MUID:88273584; PMID:2455736  
A:Accession: A32507  
A:Molecule type: mRNA  
A:Residues: 1-336 <UNN>  
C:Superfamily: calreticulin

Query Match 10.6%; Score 19; DB 2; Length 336;  
Best Local Similarity 100.0%; Pred. No. 4, 4e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKRVHVF 131  
|||||  
Db 76 IMFGPDICGPGTKRVHVF 94

RESULT 12  
A56637  
calreticulin homolog precursor - fruit fly (*Drosophila melanogaster*)  
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog  
C:Species: *Drosophila melanogaster*  
C>Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
C:Accession: A56637; A37158  
R:Smith, M.J.  
DNA Seq. 3, 247-250, 1992  
A:Title: Nucleotide sequence of a *Drosophila melanogaster* gene encoding a calreticulin  
A:Reference number: A56637; MUID:93208374; PMID:1256819  
A:Accession: A56637  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-406 <SMI>  
A:Cross-references: GB:X64461; NID:97685; PIDN:CAA5791.1; PID:97686  
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Southeimer, R.D.; Capra, J.D.  
J. Clin. Invest. 86, 332-335, 1990  
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom  
A:Reference number: A37158; MUID:90307981; PMID:2365822  
A:Accession: A37158

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
A:Molecule type: DNA  
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>  
C:Genetics:  
A:Gene: FlyBase:Crc  
A:Cross-references: FlyBase:FBgn0005585  
A:Introns: 65/1; 222/3  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 10.6%; Score 19; DB 2; Length 406;  
Best Local Similarity 100.0%; Pred. No. 5, 2e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKRVHVF 131  
|||||  
Db 130 IMFGPDICGPGTKRVHVF 148

RESULT 13  
E33208  
calreticulin, uterine - rabbit (fragment)  
C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
C>Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 01-Mar-1996  
C:Accession: E33208; F33208  
R:Miller, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; O  
J. Biol. Chem. 266, 7155-7165, 1991  
A:Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of  
A:Reference number: A33208; MUID:91201375; PMID:2016321  
A:Accession: E33208  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-29 <MIT>  
A:Note: uterine form  
A:Accession: F33208  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <MIT>  
A:Note: hepatic form  
C:Superfamily: calreticulin

Query Match 7.8%; Score 14; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1, 2e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VYFKQFLDGDGWT 17  
|||||  
Db 4 VYFKQFLDGDGWT 17

RESULT 14  
D33208  
calreticulin, brain - rabbit (fragment)  
C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
C>Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 12-Apr-1995  
C:Accession: D33208  
R:Miller, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; O  
J. Biol. Chem. 266, 7155-7165, 1991  
A:Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of  
A:Reference number: A33208; MUID:91201375; PMID:2016321  
A:Accession: D33208  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-29 <MIT>  
C:Superfamily: calreticulin

Query Match 7.8%; Score 14; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1, 2e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VYFKQFLDGDGWT 17

DB 4 VYFKQFLDGDGWT 17

RESULT 15

A48573

calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)

C:Species: Schistosoma mansoni

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A48573

R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.

Mol. Biochem. Parasitol. 57, 193-202, 1993

A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human

A:Reference number: A48573; MUID:93165070; PMID:8433712

A:Accession: A48573

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-393 <KHA>

A:Cross-references: GH:M93097; NID:9160928

A>Note: sequence inconsistent with the nucleotide translation

C:Superfamily: calreticulin

F:1-16/Domain: signal sequence #status predicted <SIG>

F:390-393/Region: endoplasmic reticulum retention signal

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 124 TKKVHYIENYKGN 137

DB 139 TKKVHYIENYKGN 152

Search completed: March 14, 2003, 20:48:58

Job time : 14.894 secs



DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE CALRETICULIN-CALCIUM binding protein (Fragments).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95143082; PubMed=7841019;  
RA Houn G., Koch C.;  
RT "Human placental calreticulin: purification, characterization and  
RT association with other proteins";  
RL Acta Chem. Scand. 48:905-911(1994).  
DR InterPro: IPR001580; Calreticulin.  
DR Prodom: PD001866; Calreticulin; 1.  
FT NON\_TER 1 1  
FT NON\_CONS 31 32  
FT NON\_CONS 59 60  
FT NON\_CONS 78 79  
FT NON\_CONS 116 117  
FT NON\_TER 214 214  
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 15.0%; Score 27; DB 4; Length 214;  
Best Local Similarity 100.0%; Pred. No. 2.4e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPAVYKQFLDGDGWTSMIESKHS 27  
Db 1 EPAVYKQFLDGDGWTSMIESKHS 27

RESULT 3  
026268 PRELIMINARY; PRT; 405 AA.

AC 026268;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin.  
GN CALRETICULIN.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93098937; PubMed=1463604;  
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;  
RT "Long-term sensitization training in Aplysia leads to an increase in  
RT calreticulin, a major presynaptic calcium-binding protein.";  
RL Neuron 9:1013-1024(1992).  
DR EMBL: S1239; AAB24569.1;  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR Prodom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DD1D69 CRC64;

Query Match 15.0%; Score 27; DB 5; Length 405;  
Best Local Similarity 100.0%; Pred. No. 4e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 YNMFPGDPCGPTKKVHYENYKGN 137  
Db 124 YNMFPGDPCGPTKKVHYENYKGN 150

RESULT 4  
ID 090650 PRELIMINARY; PRT; 421 AA.  
AC 090650;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Calreticulin precursor.  
GN CALRET.  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Susan J.M., Just M.L., Lennarz W.J.;  
RT "Cloning and characterization of Alpha Integrin and Calreticulin in  
RT Embryos of the Sea Urchin.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF177915; AAD55725.1;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR Prodom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_1; 1.  
DR PROSITE: PS00805; CALRETICULIN\_2; 1.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 421  
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41P93 CRC64;

Query Match 15.0%; Score 27; DB 5; Length 421;  
Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 YNMFPGDPCGPTKKVHYENYKGN 137  
Db 127 YNMFPGDPCGPTKKVHYENYKGN 153

RESULT 5  
09PTX7 PRELIMINARY; PRT; 318 AA.

AC 09PTX7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Calreticulin (Fragment).  
GN Lethenteron reissneri.  
OS Lethenteron reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lethenteron.  
OX NCBI\_TaxID=7753;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20063780; PubMed=10594174;  
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
RT genes.";  
RL J. Mol. Evol. 49:729-735(1999).  
DR EMBL: AB025328; BAA88481.1;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR Prodom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_1; 1.  
DR PROSITE: PS00805; CALRETICULIN\_2; 1.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.



FT NON\_TER 1 1  
SQ SEQUENCE 318 AA; 36997 MW; C88102EALCACL506 CRC64;  
Query Match 13.9%; Score 25; DB 13; Length 318;  
Best Local Similarity 100.0%; Pred. No. 4.4e-18;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 113 IMFPGDGGPSTKKVHYFENYKGN 137  
|||||  
DB 29 IMFPGDGGPSTKKVHYFENYKGN 53  
RESULT 6  
ID 016893 PRELIMINARY; PRT; 410 AA.  
AC 016893; 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-JAN-1998 (TREMBlrel. 09, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE Calreticulin.  
GN CRT-1.  
OS Amblyomma americanum.  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
OX NCBI\_TaxID=6943;  
RN [1]  
RP SEQUENCE OF 49-410 FROM N.A.  
RC TISSUE=SALIVARY GLANDS;  
RA Jaworski D.C.; Simmen F.A.; Lamoreaux W.J.; Coons L.B.; Muller M.T.;  
RT Needham G.R.;  
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
RT saliva."  
RL J. Insect Physiol. 41:369-375(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SALIVARY GLANDS;  
RA Jaworski D.C.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SALIVARY GLANDS;  
RA Fain-Thornton J.M.; Jaworski D.C.; Needham G.R.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U07708; AAC79094.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 410 AA; 47485 MW; 32C8B8750A17DC54 CRC64;  
Query Match 13.3%; Score 24; DB 5; Length 410;  
Best Local Similarity 100.0%; Pred. No. 6.3e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 73 TLVVOFTVKEQNIDCGGYYKLF 96  
|||||  
DB 89 TLVVOFTVKEQNIDCGGYYKLF 112  
RESULT 7  
ID 091711 PRELIMINARY; PRT; 343 AA.  
AC 091711; 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Calreticulin (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CNS;  
RA Treves S.; Zorzato F.; Pozzan T.;  
RT "Identification of calreticulin isoform in the CNS."  
RL Biochem. J. 0:0-0(0).  
DR EMBL: X67598; CAA47867.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
FT NON\_TER 1 1  
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA3B91DE1 CRC64;  
Query Match 12.2%; Score 22; DB 13; Length 343;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 151 FTHLYTLVPRDNTYEKIDNS 172  
|||||  
DB 140 FTHLYTLVPRDNTYEKIDNS 161  
RESULT 8  
ID 091710 PRELIMINARY; PRT; 411 AA.  
AC 091710; 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Calreticulin precursor (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CNS;  
RA Treves S.; Zorzato F.; Pozzan T.;  
RT "Identification of calreticulin isoform in the CNS."  
RL Biochem. J. 0:0-0(0).  
DR EMBL: X67597; CAA47866.1; -;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
KW Signal.  
FT NON\_TER 1 1  
FT SIGNAL <1 12 POTENTIAL.  
FT CHAIN 13 411 CALRETICULIN.  
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E0EBBEFA CRC64;  
Query Match 12.2%; Score 22; DB 13; Length 411;  
Best Local Similarity 100.0%; Pred. No. 8.4e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 151 FTHLYTLVPRDNTYEKIDNS 172  
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DB 163 FTHLYTLVPRDNTYEKIDNS 184

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RESULT 9
097372 ID 097372 PRELIMINARY; PRT; 387 AA.
AC 097372:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Calreticulin precursor.
OS Dicrofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dicrofilaria.
OX NCBI_TaxId=6287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99094497; PubMed=9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.;
RT "Molecular characterization of a calcium-binding protein from the
RT filarial parasite Dicrofilaria immitis.";
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL; AF052978; AAD03405.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; CALRETICULIN.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT CHAIN 1 18 POTENTIAL.
FT SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 11.7%; Score 21; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNIMGPDICGFGTKVHVIF 131
DB 126 YNIMGPDICGFGTKVHVIF 146

RESULT 10
096722 ID 096722 PRELIMINARY; PRT; 395 AA.
AC 096722:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Calcium binding protein calreticulin precursor.
OS Taenia solium.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Taenia.
OX NCBI_TaxId=6204;
RN [1]
RP SEQUENCE FROM N.A.
RA Mendlovic F., Ostoa-Salama P., Flisser A., Lacleite J.P.;
RT "Molecular characterization of Taenia solium calreticulin.";
RT Submitted (Jan-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF340232; AAK52725.1; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin.1.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; UNKNOWN.1.
DR PROSITE; PS00804; CALRETICULIN_2; UNKNOWN.1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; UNKNOWN.1.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
FT SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;

Query Match 11.1%; Score 20; DB 5; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VOFTVKEQNIDCGGYVKL 95
DB 92 VOFTVKEQNIDCGGYVKL 111

RESULT 11
098984 ID 098984 PRELIMINARY; PRT; 419 AA.
AC 098984:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Calreticulin.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxId=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Caenexin: its molecular cloning and expression in the liver of the
RT frog, Rana rugosa.";
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96387817; PubMed=8795287;
RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa tadpoles, but not adult frogs.";
RL J. Exp. Zool. 275:431-443(1996).
DR EMBL; D78589; BAA11425.1; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR001866; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT CHAIN 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 11.1%; Score 20; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HLYTLVPRDNTYEYKIDNS 172
DB 171 HLYTLVPRDNTYEYKIDNS 190

RESULT 12
018478 ID 018478 PRELIMINARY; PRT; 375 AA.
AC 018478:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE RAL-1 protein (Fragment).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxId=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA MacLennan K., Hoffman W.H., Taylor D.W.;
RT Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ001621; CAA04877.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin.1.

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DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; CALRETICULIN.1.  
 DR PROSITE: PS00803; CALRETICULIN.1; 1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER 375 375  
 SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 10.6%; Score 19; DB 5; Length 375;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDICGPTKKVHVF 131  
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 DB 128 IMFGPDICGPTKKVHVF 146

RESULT 13  
 O8WPG8 PRELIMINARY: PRT; 397 AA.

AC O8WPG8:  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Calreticulin.  
 OS Galleria mellonella (Max moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Pyraloidea; Pyralidae; Galleriinae; Galleria.  
 OX NCBI\_TaxID=7137;  
 RN SEQUENCE FROM N.A.  
 RC TISSUE-LARVA:  
 RA Choi J.Y., Whitten M.A., Cho M.Y., Lee K.Y., Kim M.S., Ratcliffe N.,  
 RA Lee B.L.;  
 RT "Calreticulin enriched as an early-staged encapsulation protein in wax  
 RT moth Galleria mellonella larvae: purification and molecular cloning.";  
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AB063250; BAB79277.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; CALRETICULIN.1.  
 DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN.1.  
 DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN.1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; UNKNOWN.3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
 SQ SEQUENCE 397 AA; 46024 MW; 211235D6950657F4 CRC64;

Query Match 10.6%; Score 19; DB 5; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDICGPTKKVHVF 131  
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 DB 130 IMFGPDICGPTKKVHVF 148

RESULT 14  
 O9U916 PRELIMINARY: PRT; 406 AA.

AC O9U916:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 GN CRC OR CG9429.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OREGON-R;  
 RA Dodo K., Sakoyama Y., Gamo S.;  
 RT "Drosophila melanogaster calreticulin for mRNA."  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AB000718; BAA85379.1; -;  
 DR FlyBase: FBgn005585; crc.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; CALRETICULIN.1.  
 DR PROSITE: PS00803; CALRETICULIN.1; 1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 10.6%; Score 19; DB 5; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDICGPTKKVHVF 131  
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 DB 130 IMFGPDICGPTKKVHVF 148

RESULT 15

O8WR36 PRELIMINARY: PRT; 406 AA.

AC O8WR36:  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Calreticulin.  
 OS Anopheles gambiae (African malaria mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 OC Anopheles.  
 OX NCBI\_TaxID=7165;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;  
 RT "Towards a catalog for genes and proteins from the salivary gland of  
 RT the malaria vector, Anopheles gambiae."  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF457551; AAL68781.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; CALRETICULIN.1.  
 DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN.1.  
 DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN.1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; UNKNOWN.3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
 SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9931F1 CRC64;

Query Match 10.0%; Score 18; DB 5; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 MFGPDICGPTKKVHVF 131  
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 DB 128 MFGPDICGPTKKVHVF 145

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 Job time : 26.0688 secs

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GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 8.76791 Seconds

(without alignments)  
946.243 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180  
Sequence: 1 EPAYVFKEDFLDGDGWTSRW.....PDNTEYKIDNSQVSSGLE 180

## Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

## Database :

Published Applications-AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	180	100.0	417	9	US-09-906-393A-36
2	112	6.7	12	9	US-09-906-393A-6
3	10	5.6	11	9	US-09-906-393A-5
4	9	5.0	420	10	US-09-844-006A-2
5	7	3.9	197	9	US-09-905-558C-2
6	7	3.9	446	10	US-09-850-351A-52
7	6	3.3	13	9	US-10-090-185-35
8	6	3.3	28	10	US-09-864-761-46937
9	6	3.3	31	10	US-09-823-901-8
10	6	3.3	44	10	US-09-864-761-38284
11	6	3.3	79	9	US-09-864-761-41140
12	6	3.3	94	10	US-10-178-213-266
13	6	3.3	98	10	US-09-864-761-37789
14	6	3.3	104	10	US-09-741-669-297
15	6	3.3	104	10	US-09-912-020-321
16	6	3.3	104	10	US-09-815-242-10348
17	6	3.3	116	9	US-10-078-770-128
18	6	3.3	125	9	US-10-078-770-132
19	6	3.3	161	10	US-09-815-242-13363

20	6	3.3	161	10	US-09-815-242-13615	Sequence 13615, A
21	6	3.3	218	9	US-09-925-664-14	Sequence 14, App1
22	6	3.3	218	10	US-09-189-833B-7	Sequence 7, App11
23	6	3.3	218	10	US-09-189-833B-8	Sequence 8, App11
24	6	3.3	218	10	US-09-902-705-7	Sequence 7, App11
25	6	3.3	218	10	US-09-902-705-8	Sequence 8, App11
26	6	3.3	223	10	US-09-864-761-33417	Sequence 33417, A
27	6	3.3	226	9	US-09-895-913A-362	Sequence 362, App
28	6	3.3	247	10	US-09-815-242-11342	Sequence 11342, A
29	6	3.3	247	10	US-09-815-242-11514	Sequence 11514, A
30	6	3.3	250	12	US-10-062-254-90	Sequence 90, App1
31	6	3.3	268	9	US-10-090-185-12	Sequence 14056, A
32	6	3.3	289	10	US-09-815-242-14056	Sequence 14056, A
33	6	3.3	295	10	US-09-815-242-11836	Sequence 11836, A
34	6	3.3	303	8	US-08-916-625B-4	Sequence 4, App11
35	6	3.3	311	10	US-09-815-242-13725	Sequence 13725, A
36	6	3.3	312	9	US-09-966-459A-10	Sequence 10, App1
37	6	3.3	318	10	US-09-761-569-2	Sequence 2, App11
38	6	3.3	333	9	US-09-976-059-2	Sequence 2, App11
39	6	3.3	343	10	US-09-879-017-2	Sequence 2, App11
40	6	3.3	350	9	US-10-076-754-6	Sequence 6, App11
41	6	3.3	350	9	US-10-076-773-6	Sequence 6, App11
42	6	3.3	350	10	US-09-881-752A-234	Sequence 234, App
43	6	3.3	350	12	US-10-067-615-6	Sequence 6, App11
44	6	3.3	351	9	US-10-125-692-20	Sequence 20, App11
45	6	3.3	351	10	US-09-796-033-6	Sequence 6, App11

## ALIGNMENTS

RESULT 1  
US-09-906-393A-36  
Sequence 36, Application US/09906393A  
Publication No. US20030039970A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Zhou  
APPLICANT: Xiao, Wuhan  
TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
FILE REFERENCE: 1720-1-001CIP  
CURRENT APPLICATION NUMBER: US/09/906,393A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 60/218,761  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 36  
LENGTH: 417  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-906-393A-36

Query Match 100.0%; Score 180; DB 9; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.4e-175;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKEDFLDGDGWTSRWIESKHKRSDFGKRVLSGKFGDEKDKGLQTSQDARFYAL 60  
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Db 18 EPAYVFKEDFLDGDGWTSRWIESKHKRSDFGKRVLSGKFGDEKDKGLQTSQDARFYAL 77

QY 61 SASPEFENKQTLVVOFTVKNHEQNDICGGGYVKLFNPSLDQTDHKGSEVINMGPRIC 120  
|||||  
Db 78 SASPEFENKQTLVVOFTVKNHEQNDICGGGYVKLFNPSLDQTDHKGSEVINMGPRIC 137

QY 121 GPGTKKVVIFNYKGNVLINKDKCKDEFTHTLTTLVPRDNTYEVKIDNSQVSSGLE 180  
|||||  
Db 138 GPGTKKVVIFNYKGNVLINKDKCKDEFTHTLTTLVPRDNTYEVKIDNSQVSSGLE 197

RESULT 2  
US-09-906-393A-6  
Sequence 6, Application US/09906393A  
Publication No. US20030039970A1

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;; GENERAL INFORMATION:
;; APPLICANT: Wang, Zhou
;; APPLICANT: Xiao, Wuhan
;; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
;; FILE REFERENCE: 1720-1-001CIP
;; CURRENT APPLICATION NUMBER: US/09/906,393A
;; PRIOR FILING DATE: 2001-07-16
;; PRIOR APPLICATION NUMBER: 60/218,761
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 6
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: homo sapiens
US-09-906-393A-6

Query Match          6.7%; Score 12; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 INKDIRCKDEF 151
Db 1 INKDIRCKDEF 12

RESULT 3
US-09-906-393A-5
; Sequence 5, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-906-393A-5

Query Match          5.6%; Score 10; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 CGGYVKLFP 97
Db 1 CGGYVKLFP 10

RESULT 4
US-09-844-006A-2
; Sequence 2, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
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;; SEQ ID NO 2
;; LENGTH: 420
;; TYPE: PRT
;; ORGANISM: Zea mays
US-09-844-006A-2

Query Match          5.0%; Score 9; DB 10; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 DCGGYVKL 95
Db 110 DCGGYVKL 118

RESULT 5
US-09-905-558C-2
; Sequence 2, Application US/09905558C
; Publication No. US20030024004A1
; GENERAL INFORMATION:
; APPLICANT: Garmaat, Carl W.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: zmxx1g1 Polynucleotides and Methods of
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/905,558C
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/217,942
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Zea mays
US-09-905-558C-2

Query Match          3.9%; Score 7; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 CGGYVK 94
Db 101 CGGYVK 107

RESULT 6
US-09-850-351A-52
; Sequence 52, Application US/09850351A
; Patent No. US2002010080A1
; GENERAL INFORMATION:
; APPLICANT: Feltelson, Jerald S.
; Schnepf, H. Ernest
; Narva, Kenneth E.
; Stockhoff, Brian A.
; Schmeits, James
; Loewer, David
; Dullum, Charles Joseph
; Muller-Cohn, Judy
; Stamp, Lisa
; Morrill, George
; TITLE OF INVENTION: No. US2002010080A1el Pesticidal Toxins and Nucleotide
; Sequences Which Encode These Toxins
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850.351A  
FILING DATE: 07-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 06-MAY-1998  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: PS177C8  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-850-351A-52

Query Match 3.9%; Score 7; DB 10; Length 446;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FKEQFLD 12  
DB 166 FKEQFLD 172

RESULT 7  
US-10-090-185-35  
Sequence 35, Application US/10090185  
Publication No. US20020197647A1  
GENERAL INFORMATION:  
APPLICANT: Zhang, Xiaokui  
APPLICANT: Wzrzeszczynska, Melissa H  
APPLICANT: Horvath, Curt M  
APPLICANT: Darnell Jr., James E  
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR H  
FILE REFERENCE: 600-1-253  
CURRENT APPLICATION NUMBER: US/10/090,185  
CURRENT FILING DATE: 2002-03-04  
PRIOR APPLICATION NUMBER: 09/387,418  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 35  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-090-185-35

Query Match 3.3%; Score 6; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 VQFTVK 81  
IIIIII

DB 2 VQFTVK 7

RESULT 8  
US-09-864-761-46937  
Sequence 46937, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Hank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
FILE REFERENCE: Aecmca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 46937  
LENGTH: 28  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO 295114.19  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4  
US-09-864-761-46937

Query Match 3.3%; Score 6; DB 10; Length 28;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 SASSEP 66





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;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 41140
;; LENGTH: 79
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC013751.3
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.94
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
;; OTHER INFORMATION: EST_HUMAN HIT: BE082977.1, EVALUATE 4.00e-38
;; OTHER INFORMATION: SWISSPROT HIT: O75131, EVALUATE 5.00e-39
US-09-864-761-41140
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Query Match 3.3%; Score 6; DB 10; Length 79;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 10 FLDDGC 15
Db 48 FLDDGC 53
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RESULT 12
US-10-178-213-266
;; Sequence 266, Application US/10178213
;; Publication No. US20030041348A1
;; GENERAL INFORMATION:
;; APPLICANT: Simmons, Carl R.
;; APPLICANT: Navarro Acevedo, Pedro A.
;; APPLICANT: Harvell, Leslie
;; APPLICANT: Cahoon, Rebecca
;; APPLICANT: McCutchen, Billy Fred
;; APPLICANT: Lu, Albert
;; APPLICANT: Herrmann, Rafael
;; APPLICANT: Wong, James
;; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;; FILE REFERENCE: 35718/246703
;; CURRENT APPLICATION NUMBER: US/10/178,213
;; PRIOR APPLICATION NUMBER: 60/300,152
;; PRIOR FILING DATE: 2001-06-22
;; PRIOR APPLICATION NUMBER: 60/300,241
;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 469
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 266
;; LENGTH: 94
;; TYPE: PRT
;; ORGANISM: Triticum aestivum
US-10-178-213-266
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Query Match 3.3%; Score 6; DB 9; Length 94;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 33 VLSSCK 38
```

```
Db 29 VLSSCK 34
```

```
RESULT 13
US-09-864-761-37789
;; Sequence 37789, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;; FILE REFERENCE: Aeomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263,6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 37789
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL022143.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
;; OTHER INFORMATION: EST_HUMAN HIT: AA688227.1, EVALUATE 3.00e-38
```

OTHER INFORMATION: SWISSPROT HIT: P14077, EVALUATE 1.00e-08  
US-09-864-761-37789

Query Match 3.3%; Score 6; DB 10; Length 98;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 OQLVVO 77  
| | | | |  
DB 25 OQLVVO 30

## RESULT 14

US-09-741-669-297  
Sequence 297, Application US/09741669  
Patent No. US2002022718A1  
GENERAL INFORMATION:  
APPLICANT: Forsyth, R. Allyn  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
TITLE OF INVENTION: Genes identified as required for  
FILE REFERENCE: ELITRA.009A  
CURRENT APPLICATION NUMBER: US/09/741,669  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: US 60/173005  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 481  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 297  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-741-669-297

Query Match 3.3%; Score 6; DB 10; Length 104;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 VLSSGK 38  
| | | | |  
DB 28 VLSSGK 33

## RESULT 15

US-09-912-020-321  
Sequence 321, Application US/09912020  
Patent No. US20020045592A1  
GENERAL INFORMATION:  
APPLICANT: Zyskind, Judith  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Trawick, John  
APPLICANT: Forsyth, R. Allyn  
APPLICANT: Froelich, Jamie M.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
FILE REFERENCE: ELITRA.001DV1  
CURRENT APPLICATION NUMBER: US/09/912,020  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: 09/492,709  
PRIOR FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: 60/117,405  
PRIOR FILING DATE: 1999-01-27  
NUMBER OF SEQ ID NOS: 485  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 321Z  
LENGTH: 104  
TYPE: PRT  
ORGANISM: E. coli  
US-09-912-020-321

Query Match 3.3%; Score 6; DB 10; Length 104;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 VLSSGK 38  
| | | | |  
DB 28 VLSSGK 33

Search completed: March 14, 2003, 20:51:08  
Job time : 10.7679 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 6.87679 Seconds  
(without alignments)  
1085.643 Million cell updates/sec

Title: US-09-807-148-4  
Perfect score: 180  
Sequence: 1 EPAVYKFEQFLDGDGWTSRM.....PDNTYEVKIDNSQVESGSL 180

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	100.0	417	1	CRTC_HUMAN
2	180	100.0	416	1	CRTC_MOUSE
3	77	42.8	416	1	CRTC_MOUSE
4	77	42.8	416	1	CRTC_RAT
5	62	34.4	418	1	CRTC_RABIT
6	62	34.4	400	1	CRTC_BOVIN
7	62	34.4	421	1	CRTC_BOVIN
8	19	10.6	388	1	CRTC_PIG
9	19	10.6	388	1	CRTC_PIG
10	14	7.8	393	1	CRTC_PIG
11	9	5.0	13	1	CRTC_SCHMA
12	9	5.0	24	1	CRTC_BOVIN
13	9	5.0	395	1	CRTC_CANFA
14	9	5.0	401	1	CRTC_CANFA
15	9	5.0	415	1	CRTC_EUGER
16	9	5.0	415	1	CRTC_RICCO
17	9	5.0	416	1	CRTC_BERS
18	9	5.0	416	1	CRTC_BERS
19	9	5.0	416	1	CRTC_NICPL
20	9	5.0	420	1	CRTC_CHLRE
21	9	5.0	421	1	CRTC_MAIZE
22	9	5.0	424	1	CRTC_PRUAR
23	9	5.0	424	1	CRTC_PRUAR
24	9	5.0	424	1	CRTC_ORISA
25	8	4.4	424	1	CRTC_ORISA
26	7	3.9	93	1	HMCI_METBA
27	7	3.9	93	1	HMCI_METTE
28	7	3.9	178	1	PYRE_ARCFU
29	7	3.9	183	1	PYRE_METKA
30	7	3.9	359	1	RFL_CLOAB
31	7	3.9	397	1	RPA2_PYRAB
32	7	3.9	397	1	RPA2_PYRAB
33	7	3.9	397	1	RPA2_PYRAB

34	7	3.9	414	1	PGK_SCHPO
35	7	3.9	463	1	YHCL_BACSU
36	7	3.9	591	1	CALX_MOUSE
37	7	3.9	591	1	CALX_MOUSE
38	7	3.9	592	1	CALX_MOUSE
39	7	3.9	593	1	CALX_MOUSE
40	7	3.9	681	1	MAOC_ECOLI
41	7	3.9	935	1	ITH2_PIG
42	7	3.9	1299	1	VP75_HSVSA
43	6	3.3	62	1	MRK3_XENLA
44	6	3.3	87	1	HMCB_METSO
45	6	3.3	89	1	CYC6_MONBR

## ALIGNMENTS

RESULT 1	ID	CRTC_HUMAN	STANDARD:	PRT:	417 AA.
AC	P27797				
DT	01-AUG-1992	(Rel. 23, Created)			
DT	01-AUG-1992	(Rel. 23, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HMCBP) (ERP60).				
GN	CALR OR CRTC				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92013129; PubMed=1919005;				
RA	Rochech L.A., Haselof J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,				
RA	Greene B.M., Hoch S.O.;				
RT	"Characterization of the autoantigen calreticulin.";				
RL	J. Immunol. 147:3031-3039(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90237213; PubMed=2332496;				
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,				
RA	Bachinski L.L., Itoh Y., Siciliano M.J., Retschlin M., Sonthelmer R.D.,				
RT	Capra J.D.;				
RT	"Molecular cloning, expression, and chromosome 19 localization of a				
RT	human Ro/SS-A autoantigen.";				
RL	J. Clin. Invest. 85:1379-1391(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92129342; PubMed=1733953;				
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sonthelmer R.D., Capra J.D.;				
RT	"The 5'-flanking region of the human calreticulin gene shares				
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase				
RT	promoters.";				
RL	J. Biol. Chem. 267:2557-2562(1992).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Liu J., Peng X., Yuan J., Qiang B.;				
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Lamerdin J., McCreedy P., Stliwagen S., Ramirez M., Carrano A.;				
RL	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Eye, Pancreas, and Skin;				
RA	Strausberg R.;				
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.				
RN	[7]				
RP	SEQUENCE OF 18-36.				
RX	MEDLINE=92002034; PubMed=1911778;				
RA	Roijani M.V., Finlay B.B., Gray V., Dedhar S.;				
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A				
RT	antigen (calreticulin) with a highly conserved amino acid sequence in				

RT the cytoplasmic domain of integrin alpha subunits.";  
 RL Biochemistry 30:9859-9866(1991).  
 [8]  
 RP SEQUENCE OF 18-32.  
 RX MEDLINE=90380058; PubMed=2400400;  
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;  
 RT "Sequence similarity of calreticulin with a Ca(2+)-binding protein  
 that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60  
 cells.";  
 RL Biochem. J. 270:545-548(1990).  
 [9]  
 RP SEQUENCE OF 18-28.  
 RC TISSUE=Liver;  
 RX MEDLINE=93162045; PubMed=1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 Pasquall C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargias R.,  
 Appel R.D., Hughes G.J.;  
 RT "Human liver protein map: a reference database established by  
 microsequencing and gel comparison.";  
 RL Electrophoresis 13:992-1001(1992).  
 [10]  
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
 RC TISSUE=keratinocytes;  
 RX MEDLINE=93162043; PubMed=1286667;  
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
 Vandekerckhove J.;  
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
 protein database of normal human epidermal keratinocytes.";  
 RL Electrophoresis 13:960-969(1992).  
 [11]  
 RP SEQUENCE OF 18-26.  
 RC TISSUE=Colon carcinoma;  
 RX MEDLINE=9295306; PubMed=9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
 RT "A two-dimensional gel database of human colon carcinoma proteins.";  
 RL Electrophoresis 18:605-613(1997)  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro  
 autoantigen.  
 -----  
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 or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 -----  
 DR EMBL: M84739; AAA51916.1; -;  
 DR EMBL: M32294; AAA36582.1; -;  
 DR EMBL: AY047586; AAL13126.1; -;  
 DR EMBL: AD000092; AAB51176.1; -;  
 DR EMBL: BC002500; AA02500.1; -;  
 DR EMBL: BC007911; AA07911.1; -;  
 DR EMBL: BC020493; AA020493.1; -;  
 DR PIR: A37047; A37047;  
 DR PIR: S11475; S11475;  
 DR PIR: A42330; A42330;  
 DR PIR: A46452; A46452;  
 DR SWISS-2DPAGE: P27797; HUMAN.  
 DR Aarhus/Ghent-2DPAGE: 9401; IEF.  
 DR PMMA-2DPAGE: P27797; -;  
 DR PHCI-2DPAGE: P27797; -;  
 DR HSC-2DPAGE: P27797; HUMAN.  
 DR Stena-2DPAGE: P27797; -;  
 DR Genew: HGNC:1455; CALR.  
 DR MIM: 109091; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.

DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR006626; CALRETICULIN.  
 DR Prodom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN.1; 1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN-REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 417 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISLFD 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;  
 Query Match 100.0%; Score 180; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 6,8e-178; Indels 0; Gaps 0;  
 Matches 180; Conservative 0; Mismatches 0;  
 QY 1 EPAYVFEQFLDGDGNTSMIESKHSKSDGKFEVLSSGKFEYGEEDKGLQTSQDAEFYAL 60  
 DB 18 EPAYVFEQFLDGDGNTSMIESKHSKSDGKFEVLSSGKFEYGEEDKGLQTSQDAEFYAL 77  
 QY 61 SASFEPEFSKGGTLVYQFVYKHEQNIIDCGGKYKLFPSNLDQTDHMGSEYVIMGPDIC 120  
 DB 78 SASFEPEFSKGGTLVYQFVYKHEQNIIDCGGKYKLFPSNLDQTDHMGSEYVIMGPDIC 137  
 QY 121 GGTGKVVHYIFVYKGNVLIINDIRCKDEFTLTLIYRPNTFEVKKIDNSQVESGSIE 180  
 DB 138 GGTGKVVHYIFVYKGNVLIINDIRCKDEFTLTLIYRPNTFEVKKIDNSQVESGSIE 197  
 RESULT 2  
 CRTC\_MOUSE STANDARD; PRT; 416 AA.  
 ID AC P14211;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).  
 GN CALR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.  
 RC STRAIN=BAIB/C; TISSUE=Liver;  
 RX MEDLINE=9005955; PubMed=2583110;  
 RA Smith M.J., Koch G.L.E.;  
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,  
 RT HACBP), a major calcium binding ER/SR protein.";  
 RL EMBO J. 8:3581-3586(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93013037; PubMed=1398135;  
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;  
 RT "Determination of the sequence of an expressible cDNA clone encoding  
 RT ERP60/calregulin by the use of a novel nested set method.";  
 RL Gene 120:217-225(1992).

[3]  
 RN SEQUENCE OF 18-38.  
 RP TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X14926; CA33053.1; -;  
 DR EMBL: M92988; AAA37569.1; -;  
 DR PIR: S06763; S06763.  
 DR PIR: JC1444; JC1444.  
 DR SWISS-2DPAGE: P14211; MOUSE.  
 DR MGD: MGI:88252; Calif.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PRO0626; CALRETICULIN.  
 DR Prodom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 416 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 413 416 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CNGC64;  
 Query Match 42.8%; Score 77; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-71;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P18418; P10452;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calretiquin) (HACBP) (ERP60) (CALBP)  
 DE (Calcium-binding protein 3) (CABP3).  
 GN CALR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;  
 RX MEDLINE=90370496; PubMed=2295661;  
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,  
 RA Holmes C., Patel Y.C.;  
 RT "Structural homology between the rat calreticulin gene product and  
 RT the Onchocerca volvulus antigen Ral-1.";  
 RL Nucleic Acids Res. 18:4933-4933(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=93202172; PubMed=8453984;  
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamamoto T., Arai K.,  
 RA Okinaga S., Kobayashi T.;  
 RT "An endoplasmic reticulum protein, calreticulin, is transported into  
 RT the acrosome of rat sperm.";  
 RL Exp. Cell Res. 205:101-110(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=95181573; PubMed=7876339;  
 RA Soenichsen B., Fueillekrug J., van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Mieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain  
 RT calreticulin in the endoplasmic reticulum.";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 RN [4]  
 RP SEQUENCE OF 270-358 FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Lone Y.C., Bailly A., Latruffe N.;  
 RL Submitted (Dec-1988) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 18-29.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [6]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
 RX MEDLINE=92360010; PubMed=1497655;  
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
 RT "Calreticulin is present in the acrosome of spermatozoa of rat  
 RT testis.";  
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
 RN [7]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=LEC; TISSUE=Liver;  
 RX MEDLINE=94072621; PubMed=8251535;  
 RA Yokoi T., Negayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
 RA Kametaki T.;  
 RT "Identification of protein disulfide isomerase and calreticulin as  
 RT autoimmune antigens in LEC strain of rats.";  
 RL Biochim. Biophys. Acta 1158:339-344(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC -! CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-  
 CC HYDROXYBUTYRATE DEHYDROGENASE.  
 CC -----  
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 CC -----  
 DR EMBL: D78308; BAA11345.1; -  
 DR EMBL: X53363; CAA37446.1; -  
 DR EMBL: X13702; CAA31987.1; ALT\_SEQ.  
 DR EMBL: X79327; CAA55890.1; -  
 DR PIR: S04867; S04867.  
 DR PIR: S11205; S11205.  
 DR PIR: S13045; S13045.  
 DR PIR: A49176; A49176.  
 DR PIR: S45036; S45036.  
 DR PIR: JH0819; JH0819.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin\_1.  
 DR PRINTS: PR001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum: Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416  
 FT DOMAIN 18 197  
 FT DOMAIN 198 308  
 FT DOMAIN 309 416  
 FT DOMAIN 191 255  
 FT REPEAT 191 202  
 FT REPEAT 210 221  
 FT REPEAT 227 238  
 FT REPEAT 244 255  
 FT DOMAIN 259 297  
 FT REPEAT 259 269  
 FT REPEAT 273 283  
 FT REPEAT 287 297  
 FT DOMAIN 351 407  
 FT DISULFID 137 163  
 FT SITE 413 416  
 SO SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;  
 Query Match 42.8%; Score 77; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-71;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 104 DMHGSSEYIMFGPDICGCTKKVHYIFNFKGNVLIINDIRCKDDEFHLYTLIVRPD 163  
 DB 121 DMHGSSEYIMFGPDICGCTKKVHYIFNFKGNVLIINDIRCKDDEFHLYTLIVRPD 180  
 QY 164 TVEVKIDNSOVESGLE 180  
 DB 181 TVEVKIDNSOVESGLE 197  
 RESULT 4  
 ID CRTG\_RABIT STANDARD; PRT; 418 AA.  
 AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 RX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=slow-twitch skeletal muscle;  
 RX MEDLINE=90094320; PubMed=2600080;  
 RA Fliedel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;  
 RT "Molecular cloning of the high affinity calcium-binding protein  
 RT (calreticulin) of skeletal muscle sarcoplasmic reticulum";  
 RL J. Biol. Chem. 264:21522-21528(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fast-twitch skeletal muscle;  
 RX MEDLINE=91282795; PubMed=2059224;  
 RA Fliedel L., Michalak M.;  
 RT "Fast-twitch and slow-twitch skeletal muscles express the same  
 RT isoform of calreticulin";  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 RN [3]  
 RP SEQUENCE OF 18-36.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain";  
 RL Biochem. J. 271:473-480(1990).  
 RN [4]  
 RP SEQUENCE OF 18-46.  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=92002038; PubMed=1911780;  
 RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 RT monooxygenase and calreticulin";  
 RL Biochemistry 30:9892-9900(1991).  
 CC -! FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -! SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -! SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -! SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: J05138; AAA31188.1; -  
 DR PIR: A34154; A34154.  
 DR PIR: C33208; C33208.  
 DR PIR: D33208; D33208.  
 DR PIR: E33208; E33208.  
 DR PIR: F33208; F33208.  
 DR PIR: S13046; S13046.  
 DR PIR: S13047; S13047.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin\_1.  
 DR PRINTS: PR00626; Calreticulin.  
 DR Prodom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.

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DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SO SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 42.8%; Score 77; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1,1e-71;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSYINMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLIVRPDN 163
DB 121 DMHGDSYINMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLIVRPDN 180
QY 164 TYEVKIDNSQVSSGLE 180
DB 181 TYEVKIDNSQVSSGLE 197

RESULT 5
CRT1_BOVIN
ID CRT1_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94183174; PubMed=8135753;
RA Matsuno K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin."
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.

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FT DOMAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146 N-LINKED (GLCNAc. . .).
FT CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).
FT SITE 397 400 7D4B6D6FC689BEF1 CRC64;
SO SEQUENCE 400 AA; 46381 MW; 7D4B6D6FC689BEF1 CRC64;

Query Match 34.4%; Score 62; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 3,1e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTMHGDSYINMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLIV 159
DB 100 LDQTMHGDSYINMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLIV 159
QY 160 RP 161
DB 160 RP 161

RESULT 6
CRT2_BOVIN
ID CRT2_BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin."
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L13462; AAC37307.1; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.

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DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 34  
 FT CHAIN 35 421  
 FT DOMAIN 35 201  
 FT DOMAIN 202 312  
 FT DOMAIN 313 421  
 FT DOMAIN 195 259  
 FT REPEAT 195 206  
 FT REPEAT 214 225  
 FT REPEAT 231 242  
 FT REPEAT 248 259  
 FT DOMAIN 263 301  
 FT REPEAT 263 273  
 FT REPEAT 277 287  
 FT REPEAT 291 301  
 FT DOMAIN 366 411  
 FT DISULFID 141 167  
 FT CARBOHYD 183 183  
 FT SITE 418 421  
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match  
 Best Local Similarity 100.0%; Pred. No. 3.3e-56; Length 421;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDPTDHGSEYINMGPGICGPTKKVIVFNFKGNVILINDICRDEFTHTLTLY 159  
 DB 121 LDPTDHGSEYINMGPGICGPTKKVIVFNFKGNVILINDICRDEFTHTLTLY 180

QY 160 RP 161  
 DB 181 RP 182

RESULT 7  
 CRTC\_PIG STANDARD; PRT; 105 AA.  
 AC P28491;  
 DT 01-DEC-1992 (rel. 24, Created)  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 01-NOV-1997 (rel. 35, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60) (Fragment).  
 GN CALR.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Small intestine;  
 RX MEDLINE=96327607; PubMed=8672129;  
 RA Wintere A.K., Fredholm M., Davies W.;  
 RT "Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones."  
 RL Mamm. Genome 7:509-517(1996).  
 RN [2]  
 RP SEQUENCE OF 18-32.  
 RC TISSUE=uterus;  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Bakesh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calnexin, is the major calcium binding protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic reticulum."  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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 CC -----  
 DR EMBL: F14591; CA423142.1; -.  
 DR PIR: B33208; B33208.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; PARTIAL.  
 DR PROSITE: PS00804; CALRETICULIN\_2; PARTIAL.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 >105  
 FT DOMAIN 18 >105  
 FT NON\_TER 105 105  
 SQ SEQUENCE 105 AA; 11958 MW; D203B53FE36BDE1E CRC64;

Query Match  
 Best Local Similarity 13.9%; Score 25; DB 1; Length 105;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 FEFPNKGOTLVQFTVKEHQNIDC 88  
 DB 81 FEFPNKGOTLVQFTVKEHQNIDC 105

RESULT 8  
 RAL1\_ONCOV STANDARD; PRT; 388 AA.  
 AC P11012;  
 DT 01-JUL-1989 (rel. 11, Created)  
 DT 01-NOV-1995 (rel. 32, Last sequence update)  
 DT 01-OCT-1996 (rel. 34, Last annotation update)  
 DE RAL-1 protein precursor (41 kDa larval antigen).  
 GN RAL1.  
 OS Onchocerca volvulus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 CC Onchocercidae; Onchocerca.  
 OX NCBI\_Taxid=6282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94341871; PubMed=7520419;  
 RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;  
 RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the calreticulin family of proteins, recognized by sera from patients with onchocerciasis."  
 RL Infect. Immun. 62:3696-3704(1994).  
 RN [2]  
 RP SEQUENCE OF 53-388 FROM N.A.  
 RX MEDLINE=88273584; PubMed=2455736;  
 RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;  
 RT "Isolation and characterization of expression cDNA clones encoding antigens of Onchocerca volvulus infective larvae."  
 RL J. Clin. Invest. 82:262-269(1988).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M20565; AAA59056.1; -.  
 DR PIR: A32507; A32507.



DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin. 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin. 1.  
 DR PROSITE: PS00803; CALRETICULIN.1; 1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT. 3.  
 KW Calcium-binding; Repeat; Antigen; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 388 RAL-1 PROTEIN.  
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
 FT REPEAT 189 200 1-1.  
 FT REPEAT 208 219 1-2.  
 FT REPEAT 225 236 1-3.  
 FT REPEAT 242 253 1-4.  
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
 FT REPEAT 257 267 2-1.  
 FT REPEAT 271 281 2-2.  
 FT REPEAT 285 295 2-3.  
 FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
 FT DISULFID 135 161 BY SIMILARITY  
 FT SEQUENCE 388 AA; 45298 MM; 9537F298A2D31CD6 CRC64;  
 Query Match 10.6%; Score 19; DB 1; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 6,7e-12;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 113 IMFGDPCGPGTKVHVIF 131  
 Db 128 IMFGDPCGPGTKVHVIF 146

RESULT 9  
 CRTC\_DROME STANDARD: PRT; 406 AA.  
 AC P29413; Q9VHA3;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-OCT-1993 (Rel. 27, Last annotation update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).  
 GN CRC OR CG9429.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93208374; PubMed=1296819;  
 RA Smith M.J.;  
 RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a  
 calreticulin homologue.";  
 RL DNA Seq. 3:247-250(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Mortan J.R., Yandell M.D., Zhang O., Chen L.X.,  
 Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,  
 Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 Jafali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pachet J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP SEQUENCE OF 91-124 AND 182-220.  
 RX MEDLINE=90307981; PubMed=2365822;  
 RA McCulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sonthelmer R.D.,  
 Capra J.D.;  
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
 highly homologous with onchocercal RAL-1 antigen and an alysia  
 'memory molecule'.";  
 RT J. Clin. Invest. 86:332-335(1990).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
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 CC -----  
 DR EMBL: X64461; CA45791.1; -;  
 DR EMBL: AE003683; AAF54416.1; -;  
 DR PIR: A37158; A37158.  
 DR FlyBase: FBgn0005585; Crc.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin. 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin. 1.  
 DR PROSITE: PS00014; ER-TARGET. 1.  
 DR PROSITE: PS00803; CALRETICULIN.1; 1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT. 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 406 CALRETICULIN.  
 FT CONFLICT 107 107 G -> A (IN REF. 3).  
 FT CONFLICT 184 184 V -> L (IN REF. 3).  
 FT SEQUENCE 406 AA; 46808 MM; 65D72C69D0BEC427 CRC64;  
 Query Match 10.6%; Score 19; DB 1; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 7e-12;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 113 IMFGDPCGPGTKVHVIF 131  
 Db 130 IMFGDPCGPGTKVHVIF 148

RESULT 10  
 CRTC\_CANFA STANDARD; PRT; 393 AA.  
 AC 006814; Q26562;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Calreticulin precursor (SM4 protein).  
 OS Schistosoma mansoni (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Puerto Rican;  
 RX MEDLINE=93165070; PubMed=8433712;  
 RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,  
 Capron A.;  
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen  
 homologous to human Ro/SS-A autoantigen";  
 RL Mol. Biochem. Parasitol. 57:193-202(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Puerto Rican;  
 RX MEDLINE=94187805; PubMed=8139623;  
 RA Khalife J., Pierce R.J., Godin C., Capron A.;  
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni  
 calreticulin";  
 RL Mol. Biochem. Parasitol. 62:313-315(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 -1- LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL: M93097; AAA29854.1; -  
 DR EMBL: U24159; AAA19024.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 16  
 FT CHAIN 17 393  
 FT DOMAIN 189 254  
 FT REPEAT 189 200  
 FT REPEAT 209 220  
 FT REPEAT 225 236  
 FT REPEAT 243 254  
 FT DOMAIN 257 295  
 FT REPEAT 257 267  
 FT REPEAT 271 281  
 FT REPEAT 285 295  
 FT REPEAT 295 300  
 FT DISULFID 135 161  
 FT SITE 390 393  
 FT CONFLICT 89 90  
 FT CONFLICT 188 207  
 FT CONFLICT 378 378  
 FT SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 7.8%; Score 14; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 124 TRKWHVIFNFKGN 137  
 DB 139 TRKWHVIFNFKGN 152  
 RESULT 11  
 CRTC\_BOVIN STANDARD; PRT; 13 AA.  
 AC P28489;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin (CRP55) (Calregulin) (HACBP) (Erp60) (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 reticulum";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 -1- LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 DR PIR: A33208; A33208.  
 DR InterPro: IPR001580; Calreticulin.  
 DR PROSITE: PS00803; CALRETICULIN\_1; PARTIAL.  
 DR PROSITE: PS00804; CALRETICULIN\_2; PARTIAL.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding.  
 FT NON\_TER 13 13  
 FT SEQUENCE 13 AA; 1557 MW; C85DDA6993CA1339 CRC64;  
 Query Match 5.0%; Score 9; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0091;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 YFKEQFLDG 13  
 DB 5 YFKEQFLDG 13  
 RESULT 12  
 CRTC\_CANFA STANDARD; PRT; 24 AA.  
 AC P28490;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin (CRP55) (Calregulin) (HACBP) (Erp60) (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RA Michalak M., Baksh S., Opas M.;  
 RT Submitted (JUL-1991) to the PIR data bank.

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CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR PIR: A39143; A39143.
DR InterPro: IPR001580; Calreticulin.
DR PROSITE: PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE: PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON-TER 24
SQ SEQUENCE 24 AA; 2852 MW; D5C76F2CB94B5C40 CRC64;

Query Match 5.0%; Score 9; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YFKEQFLDG 13
Db 5 YFKEQFLDG 13

RESULT 13
CRTC_CAEEL STANDARD; PRT; 395 AA.
ID CRTC_CAEEL
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
GN CRT-1 OR Y38A10A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=9232978; PubMed=1627827;
RA Smith M.J.;
RT "A. C. elegans gene encodes a protein homologous to mammalian
RT calreticulin."
RL DNA Seq. 2:235-240(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Bauer C.; Courtney L.; Laplant Y.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC -----
DR EMBL: X59589; CAA42159.1; -.
DR EMBL: AF125963; AAD14746.1; -.
DR PIR: S25851; S25851.
DR WormPep: Y38A10A.5; CE21562.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.

```

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DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.
FT SIGNAL 1 15
FT CHAIN 16 395
FT DOMAIN 7 192
FT DOMAIN 193 301
FT DOMAIN 302 395
FT DOMAIN 186 250
FT REPEAT 186 197
FT REPEAT 205 216
FT REPEAT 222 233
FT REPEAT 239 250
FT REPEAT 254 292
FT REPEAT 254 264
FT REPEAT 268 278
FT REPEAT 282 292
FT DOMAIN 332 390
FT DISULFID 133 158
FT SITE 392 395
SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;

Query Match 5.0%; Score 9; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 IDCGGYVK 94
Db 99 IDCGGYVK 107

RESULT 14
CRTC_EUGGR STANDARD; PRT; 401 AA.
ID CRTC_EUGGR
AC Q92NT3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Euglena gracilis.
OS Euglena gracilis.
OC Eukaryota; Euklenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP SEQUENCE FROM N.A.
RA Navazro L.; Balzan B.; Martin W.; Mariani P.;
RT "Evidence for conservation of a calcium homeostatic component:
RT purification, characterization and cloning of calreticulin from Euglena
RT gracilis."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (by similarity).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y09816; CAA70945.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.

```

DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; FALSE\_NEG.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 401  
 FT SITE 398 401  
 FT SEQUENCE 401 AA; 45910 MW; 056B074C16292674 CRC64;  
 PREVENT SECRETION FROM ER (POTENTIAL).

OY 113 IMFGPDIG 121  
 DB 131 IMFGPDIG 139

Search completed: March 14, 2003, 20:45:05  
 Job time : 8.87679 secs

Query Match 5.0%; Score 9; DB 1; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDIG 121  
 DB 127 IMFGPDIG 135

## RESULT 15

CRTC\_RICCO STANDARD; PRT; 415 AA.

AC P93508;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 OS Ricinus communis (Castor bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
 CX NCBI\_TaxID=3998;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97435975; PubMed=9290642;  
 RA Coughlan S.J., Hastings C., Winfrey R. Jr.;  
 RT "Cloning and characterization of the calreticulin gene from Ricinus communis L.";  
 RL Plant Mol. Biol. 34:897-911(1997).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----

DR EMBL: U74631; AAB71420.1; -;  
 DR EMBL: U74630; AAB71419.1; -;  
 DR InterPro: IPR001580; Calreticulin;  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 20  
 FT CHAIN 21 415  
 FT CARBOHD 52 52  
 FT CARBOHD 152 152  
 FT SITE 412 415  
 FT SEQUENCE 415 AA; 47522 MW; DD5F452E76CCTF8C CRC64;  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 PREVENT SECRETION FROM ER (POTENTIAL).

Query Match 5.0%; Score 9; DB 1; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 29.8711 Seconds  
(without alignments)  
1342.037 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 417

Sequence: 1 MLTSVPLLLGLGLAVALPEA.....EDKEDDEEDVPGAKDEL 417

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	417	100.0	417	1 A37047	calreticulin precu
2	182	43.6	418	1 A34134	calreticulin precu
3	93	22.3	416	1 S06763	calreticulin precu
4	93	22.3	416	2 JH0819	calreticulin precu
5	62	14.9	400	2 S43376	calreticulin, brai
6	62	14.9	421	2 S36799	calreticulin precu
7	39	9.4	411	2 S29129	calreticulin precu
8	27	6.5	405	1 JH0795	calreticulin precu
9	23	5.5	336	2 A32507	41K larval antigen
10	22	5.3	384	2 S29130	calreticulin (clon
11	20	4.8	419	2 S71343	calreticulin precu
12	19	4.6	406	2 A56637	calreticulin homol
13	17	4.1	395	2 S25851	calreticulin precu
14	14	3.4	29	2 E33208	calreticulin, uter
15	14	3.4	29	2 D33208	calreticulin, brai
16	14	3.4	393	1 A48573	calreticulin autoa
17	13	3.1	178	2 S26481	calreticulin binding pr
18	13	3.1	415	2 T10172	calreticulin - cas
19	13	3.1	421	2 S58170	calreticulin precu
20	12	2.9	27	2 PC2299	calreticulin - Chi
21	11	2.6	15	2 B33208	calreticulin, uter
22	11	2.6	24	2 A33434	calcium-binding pr
23	11	2.6	29	2 C33208	calreticulin, slow
24	11	2.6	389	2 T03691	calreticulin - com
25	11	2.6	412	2 T05703	calreticulin - bar
26	11	2.6	415	2 T05705	calreticulin - bar
27	11	2.6	416	2 T16968	calreticulin call
28	11	2.6	422	2 T07841	probable calreticu
29	11	2.6	428	2 T03251	calnexin - maize (

30	11	2.6	530	2 JN0597	calnexin-like prot
31	11	2.6	532	2 T49873	calnexin homolog -
32	11	2.6	540	2 T10892	probable calnexin
33	11	2.6	546	2 T06415	calnexin - soybean
34	10	2.4	132	2 H75548	hypothetical prote
35	9	2.2	13	2 A33208	calreticulin, hepa
36	9	2.2	15	2 G60977	protein 425 - Call
37	9	2.2	24	2 A61141	calreticulin, panc
38	9	2.2	77	2 A63343	hypothetical prote
39	9	2.2	149	2 S39556	high mobility grou
40	9	2.2	361	2 S68268	apurinic/apurimid
41	9	2.2	372	2 T04266	hypothetical prote
42	9	2.2	412	2 A55320	immunophilin FKBP4
43	9	2.2	416	2 T14554	calreticulin - bee
44	9	2.2	425	2 C96605	calreticulin (Crl)
45	9	2.2	444	2 H86224	hypothetical prote

## ALIGNMENTS

RESULT 1  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sonthelmer, R.D.; Capra, J.D.  
J. Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
A:Reference number: A42330; MUID:92129342; PMID:1733953  
A:Accession: A42330  
A:Molecule type: DNA  
A:Residues: 1-417 <MC2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:78536)  
R:McCaulliffe, D.P.; Lux, F.A.; Liew, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
J. Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
A:Reference number: A37047; MUID:90237213; PMID:2332496  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MCC>  
A:Cross-references: GB:M47394; NID:9337486; PIDN:AAA36582.1; PID:9337487  
A:Note: The authors translated the codon GGA for residue 349 as Tyr  
R:Roach, L.A.; Haselby, J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.  
J. Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129; PMID:1919005  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <RKC>  
A:Cross-references: GB:M47394; NID:9179881; PIDN:AAA51916.1; PID:9179882  
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBI:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sonthelmer, R.D.  
J. Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence  
A:Reference number: A28812; MUID:88273610; PMID:3260607  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LIE>  
A:Note: 18-Ala was also found  
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.  
J. Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
A:Reference number: PH1525; MUID:93115648; PMID:8418194  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DUP>  
A:Experimental source: LAK cell  
R:Rojanian, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

A:Reference number: A40346; MUID:92002034; PMID:1911778  
 A:Accession: A40346  
 A:Molecule type: protein  
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin)  
 A:Reference number: A34154; MUID:90094320; PMID:2600080  
 A:Accession: A34154  
 A:Molecule type: mRNA  
 A:Status: preliminary  
 A:Residues: 1-418 <FL>  
 A:Cross-references: GB:J05138; NID:9164858; PIDN:AAA31188.1; PID:9164859  
 A:References: S. de Mattei, M.; Lantredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
 Biochem. J. 271, 473-480, 1990  
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
 A:Reference number: S13045; MUID:91054414; PMID:2241926  
 A:Accession: S13047  
 A:Molecule type: protein  
 A:Residues: 19-32 <TR>  
 A:Superfamily: calreticulin  
 C:Keywords: skeletal muscle  
 F:1-17/Domain: signal sequence #status predicted <Sig>  
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 43.6%; Score 182; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 3e-163;  
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DMHGDSEYNMFPGDPCGPTKKVHVIFNFKGNVLIINKDIRCKDEFTHTLYLTPDN 180  
 DB 121 DMHGDSEYNMFPGDPCGPTKKVHVIFNFKGNVLIINKDIRCKDEFTHTLYLTPDN 180  
 QY 181 TYEVKIDNSQVESGSLDDMDFLPPKKIKDPDASKPEMDERAKIDPPTDSKPEMDKPE 240  
 DB 181 TYEVKIDNSQVESGSLDDMDFLPPKKIKDPDASKPEMDERAKIDPPTDSKPEMDKPE 240  
 QY 241 HIPDPAPKRPEDMDGEMEPVYQNPYKEMKPRQIDNDYGTWTHPEIDNPEYS 300  
 DB 241 HIPDPAPKRPEDMDGEMEPVYQNPYKEMKPRQIDNDYGTWTHPEIDNPEYS 300  
 QY 301 PDPSIAYDNFVGLDLMQVKSCTTFDNFLINDEAYAEFENFMWGYTAAEKQMKDK 360  
 DB 301 PDPSIAYDNFVGLDLMQVKSCTTFDNFLINDEAYAEFENFMWGYTAAEKQMKDK 360  
 QY 361 ODEQRLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417  
 DB 361 ODEQRLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417

RESULT 2  
 A34154  
 calreticulin precursor, skeletal muscle - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999  
 C:Accession: A34154; S13047

R.Fliegell, L.; Burns, K.; MacLennan, D.H.; Reilmeyer, R.A.F.; Michalak, M.  
 J. Biol. Chem. 264, 21522-21528, 1989  
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin)  
 A:Reference number: A34154; MUID:90094320; PMID:2600080  
 A:Accession: A34154  
 A:Molecule type: mRNA  
 A:Status: preliminary  
 A:Residues: 1-418 <FL>  
 A:Cross-references: GB:J05138; NID:9164858; PIDN:AAA31188.1; PID:9164859  
 A:References: S. de Mattei, M.; Lantredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
 Biochem. J. 271, 473-480, 1990  
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
 A:Reference number: S13045; MUID:91054414; PMID:2241926  
 A:Accession: S13047  
 A:Molecule type: protein  
 A:Residues: 19-32 <TR>  
 A:Superfamily: calreticulin  
 C:Keywords: skeletal muscle  
 F:1-17/Domain: signal sequence #status predicted <Sig>  
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 43.6%; Score 182; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 3e-163;  
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DMHGDSEYNMFPGDPCGPTKKVHVIFNFKGNVLIINKDIRCKDEFTHTLYLTPDN 180  
 DB 121 DMHGDSEYNMFPGDPCGPTKKVHVIFNFKGNVLIINKDIRCKDEFTHTLYLTPDN 180  
 QY 181 TYEVKIDNSQVESGSLDDMDFLPPKKIKDPDASKPEMDERAKIDPPTDSKPEMDKPE 240  
 DB 181 TYEVKIDNSQVESGSLDDMDFLPPKKIKDPDASKPEMDERAKIDPPTDSKPEMDKPE 240  
 QY 241 HIPDPAPKRPEDMDGEMEPVYQNPYKEMKPRQIDNDYGTWTHPEIDNPEYS 300  
 DB 241 HIPDPAPKRPEDMDGEMEPVYQNPYKEMKPRQIDNDYGTWTHPEIDNPEYS 300  
 QY 301 PDPSIAYDNFVGLDLMQVKSCTTFDNFLINDEAYAEFENFMWGYTAAEKQMKDK 360  
 DB 301 PDPSIAYDNFVGLDLMQVKSCTTFDNFLINDEAYAEFENFMWGYTAAEKQMKDK 360  
 QY 361 ODEQRLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417  
 DB 361 ODEQRLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417

RESULT 3  
 S06763  
 calreticulin precursor - mouse  
 N:Alternate names: 55K calcium-binding reticuloplasmic; calregulin  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999  
 C:Accession: S06763; JCI444; PC1233; A57498  
 R:Smith, M.J.; Koch, G.L.E.  
 EMBO J. 8, 3581-3586, 1989  
 A:Title: Multiple zones in the sequence of calreticulin (CRP5, calregulin, HACBP), a  
 A:Reference number: S06763; MUID:90059955; PMID:2583110  
 A:Accession: S06763  
 A:Molecule type: DNA  
 A:Residues: 1-416 <SM>  
 A:Cross-references: EMBL:X14926; NID:950567; PIDN:CAA33053.1; PID:950568  
 R:Mazarella, R.A.; Gold, P.; Cunningham, M.; Green, M.  
 Gene 120, 217-225, 1992  
 A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca  
 A:Reference number: JCI444; MUID:93013037; PMID:1398135  
 A:Accession: JCI444  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <MAZ>  
 A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085  
 A:Accession: PC1233  
 A:Molecule type: protein  
 A:Residues: 18-41 <MAZ>  
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.  
 J. Biol. Chem. 270, 15926-15929, 1995  
 A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mous  
 A:Reference number: A57498; MUID:95332280; PMID:7608143  
 A:Accession: A57498

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A:Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHT>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match      22.3%; Score 93; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 DMHGSEYNIMFGPDICPGTKKVVIFNYKGNVLIKDKRCDEFTHTLTVLRPDN 180

Qy 181 TYEVKIDNSQVESGSLIEDMDFLPPKIKDPDA 213
Db 181 TYEVKIDNSQVESGSLIEDMDFLPPKIKDPDA 213

RESULT 4
JH0819
calreticulin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
A:Accession: JH0819; A49176; S11205; S45036; S04867; S39372; A34473; S13045
R:Nakamura, M.; Moriya, A.; Baba, T.; Michikawa, Y.; Yamanohe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
A:Reference number: A49176; MUID:93202172; PMID:8453984
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
A:Accession: A49176
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells
A:Note: sequence extracted from NCBI backbone (NCBI:127639, NCBI:127643)
R:Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y
Nucleic Acids Res. 18, 4933, 1990
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc
A:Reference number: S11205; MUID:90370496; PMID:2395661
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:955854; PIDN:CA537446.1; PID:g55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A:Title: Calreticulin is present in the acrosome of spermatis of rat testis.
A:Reference number: PC1109; MUID:92360010; PMID:1497655
A:Accession: PC1109
A:Molecule type: protein
A:Residues: 18-32 <NAK>
A:Experimental source: testis, strain Sprague-Dawley
R:Soenlichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
submitted to the EMBL Data Library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticuli
A:Reference number: S45036
A:Accession: S45036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOE>
A:Cross-references: EMBL:X79327; NID:9488840; PIDN:CA55890.1; PID:g488841
R:Lone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A:Reference number: S04867
A:Accession: S04867

A:Molecule type: mRNA
A:Residues: 'R',270-358,'AAG',<LON>
A:Cross-references: EMBL:X13702; NID:956055; PIDN:CA531987.1; PID:g930260
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horinuchi, R.; Kametaki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune
A:Reference number: S39371; MUID:94072621; PMID:8251535
A:Accession: S39372
A:Molecule type: protein
A:Residues: 18-23,'X',25-32 <YOK>
R:Van, P.N.; Peter, F.; Soeling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes
itive calcium sequestering rat liver vesicles.
A:Reference number: A34473; MUID:9008920; PMID:2793869
A:Accession: A34473
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Reves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13045
A:Molecule type: protein
A:Residues: 18-29 <TRE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:204-212/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match      22.3%; Score 93; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 DMHGSEYNIMFGPDICPGTKKVVIFNYKGNVLIKDKRCDEFTHTLTVLRPDN 180
Db 121 DMHGSEYNIMFGPDICPGTKKVVIFNYKGNVLIKDKRCDEFTHTLTVLRPDN 180

Qy 181 TYEVKIDNSQVESGSLIEDMDFLPPKIKDPDA 213
Db 181 TYEVKIDNSQVESGSLIEDMDFLPPKIKDPDA 213

RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
A:Accession: S43376; S36801
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isohe, T.
Biochem. J. 296, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63,'E',65-83 <LIO>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
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Query Match 5.5%; Score 23; DB 2; Length 336;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 232 KPEDMDKPEHIPPDPAPKPEDMD 254  
Db 178 KPEDMDKPEHIPPDPAPKPEDMD 200

## RESULT 10

S29130  
calreticulin (clone 8) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29130; T01068  
R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997; PMID:1445218  
A:Accession: S29130  
A:Molecule type: mRNA  
A:Residues: 1-384 <TR>  
A:Cross-references: EMBL:X67598  
A:Accession: T01068  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-339, 'XTGR' <TRW>  
A:Cross-references: EMBL:X67598; NID:964610; PID:CAAA7867.1; PID:954611  
A:Experimental source: CNS  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:381-384/Region: endoplasmic reticulum retention signal  
F:316/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 5.3%; Score 22; DB 2; Length 384;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 FTHLYTLVPRDNTYEKIDNS 189  
Db 140 FTHLYTLVPRDNTYEKIDNS 161

## RESULT 11

S71343  
calreticulin precursor - Korean frog  
C:Species: Rana rugosa (Korean frog)  
C>Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Jun-2000  
C:Accession: S71343  
R:Yamamoto, S.; Nakamura, M.  
FEBS Lett. 387, 27-32, 1996  
A:Title: Calnein: its molecular cloning and expression in the liver of the frog, Rana  
A:Reference number: S71342; MUID:96234004; PMID:8654561  
A:Accession: S71343  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-419 <YTA>  
A:Cross-references: EMBL:D76589; NID:91514956; PID:BAAI1425.1; PID:91514957  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-419/Product: calreticulin #status predicted <MAT>  
F:205-213/Region: nuclear location signal  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 4.8%; Score 20; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 HLTYLIVRPDNTYEKIDNS 189  
Db 171 HLTYLIVRPDNTYEKIDNS 190

## RESULT 12

A56637  
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)  
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog  
C:Species: Drosophila melanogaster  
C>Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
C:Accession: A56637; A37158  
R:Smith, M.J.  
DNA Seq. 3, 247-250, 1992  
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticuli  
A:Reference number: A56637; MUID:93208374; PMID:1296819  
A:Accession: A56637  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-406 <SMI>  
A:Cross-references: GB:X64461; NID:97685; PID:CAAA5791.1; PID:97686  
A:Note: sequence extracted from NCBI backbone (NCBI:128274, NCBI:128275)  
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sonthmeier, R.D.; Capra, J.D.  
J. Clin. Invest. 86, 332-335, 1990  
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly h  
A:Reference number: A37158; MUID:90307981; PMID:2365822  
A:Accession: A37158  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
A:Molecule type: DNA  
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>  
C:Genetics:  
A:Gene: FlyBase:Crc  
A:Cross-references: FlyBase:FBgn0005585  
A:Introns: 65/1; 222/3  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 4.6%; Score 19; DB 2; Length 406;  
Best Local Similarity 100.0%; Pred. No. 9.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 IMFPGDGGPGTKKHVIF 148  
Db 130 IMFPGDGGPGTKKHVIF 148

## RESULT 13

S25851  
calreticulin precursor - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S25851; T33996  
R:Smith, M.J.  
DNA Seq. 2, 235-240, 1992  
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.  
A:Reference number: S25851; MUID:92329978; PMID:1627827  
A:Accession: S25851  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <SMI>  
A:Cross-references: EMBL:X59589; NID:96693; PID:CAAA24159.1; PID:96694  
R:Bauer, C.; Courtney, L.; Laplant, Y.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid Y38A10A.  
A:Reference number: Z21453  
A:Accession: T33996  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-395 <BAU>  
A:Cross-references: EMBL:AF125963; PID:AAID14746.1; GSPDB:GN00023; CESP:Y38A10A.5  
A:Experimental source: strain Bristol N2; clone Y38A10A  
C:Genetics:  
A:Gene: CESP:Y38A10A.5  
A:Map position: 5

A:Introns: 107/3: 315/3  
 C:Superfamily: calreticulin  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:392-395/Region: endoplasmic reticulum retention signal

Query Match 4.1%; Score 17; DB 2; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 KPEHPPDPKKRPEDWD 254  
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 DB 233 KPEHPPDPKKRPEDWD 249

## RESULT 14

E33208  
 calreticulin, uterine - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 01-Mar-1996  
 C:Accession: E33208; F33208  
 R:Miller, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; Opas  
 J. Biol. Chem. 266, 7155-7165, 1991  
 A:Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of sm  
 A:Reference number: A33208; MUID:91201375; PMID:2016321  
 A:Accession: E33208

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-29 <MIL>  
 A:Note: uterine form  
 A:Accession: F33208  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <MI2>  
 A:Note: hepatic form  
 C:Superfamily: calreticulin

Query Match 3.4%; Score 14; DB 2; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VFKEQFLDGDGWT 34  
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 DB 4 VFKEQFLDGDGWT 17

## RESULT 15

D33208  
 calreticulin, brain - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 12-Apr-1995  
 C:Accession: D33208  
 R:Miller, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; Opas  
 J. Biol. Chem. 266, 7155-7165, 1991  
 A:Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of sm  
 A:Reference number: A33208; MUID:91201375; PMID:2016321  
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 DB 4 VFKEQFLDGDGWT 17

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GenCore version 5.1.4\_p5\_4578  
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OW protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 10.1433 seconds

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Title: US-09-807-148-4

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Word size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	11	6.1	12	US-08-045-261-4	Sequence 4, Appl
5	10	5.6	12	US-08-045-261-3	Sequence 3, Appl
6	10	5.6	12	US-08-045-261-5	Sequence 5, Appl
7	10	5.6	12	US-08-045-261-6	Sequence 6, Appl
8	9	5.0	11	US-08-675-816-2	Sequence 2, Appl
9	9	3.9	410	US-08-471-033-40	Sequence 40, Appl
10	7	3.9	410	US-08-471-033-43	Sequence 43, Appl
11	7	3.9	410	US-08-471-044-40	Sequence 40, Appl
12	7	3.9	410	US-08-471-044-43	Sequence 43, Appl
13	7	3.9	410	US-08-463-483A-40	Sequence 40, Appl
14	7	3.9	410	US-08-463-483A-43	Sequence 43, Appl
15	7	3.9	410	US-08-471-046A-40	Sequence 40, Appl
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17	7	3.9	410	US-08-470-566B-40	Sequence 40, Appl
18	7	3.9	410	US-08-470-566B-43	Sequence 43, Appl
19	7	3.9	410	US-08-469-334-40	Sequence 40, Appl
20	7	3.9	410	US-08-469-334-43	Sequence 43, Appl
21	7	3.9	410	US-09-300-529-40	Sequence 40, Appl
22	7	3.9	410	US-09-300-529-43	Sequence 43, Appl
23	7	3.9	446	US-08-960-780-52	Sequence 52, Appl
24	7	3.9	446	US-09-073-898-52	Sequence 52, Appl
25	7	3.9	449	US-08-471-033-46	Sequence 46, Appl
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34	7	3.9	462	2	US-08-463-483A-2	Sequence 2, Appl
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36	7	3.9	462	2	US-08-470-566B-2	Sequence 2, Appl
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38	7	3.9	462	3	US-09-300-529-2	Sequence 2, Appl
39	7	3.9	593	1	US-08-296-362-2	Sequence 2, Appl
40	7	3.9	1009	4	US-09-693-146-4	Sequence 4, Appl
41	7	3.9	1338	1	US-08-471-033-50	Sequence 50, Appl
42	7	3.9	1338	2	US-08-471-044-50	Sequence 50, Appl
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## ALIGNMENTS

RESULT 1  
US-08-946-026-53  
; Sequence 53, Application US/08946026  
; Patent No. 6034218  
GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Twardzik, Daniel R.  
; APPLICANT: Mitcham, Jennifer L.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/946,026  
; FILING DATE: 07-OCT-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Makl, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121, 424C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-946-026-53  
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Best Local Similarity 100.0%; Pred. No. 8.3e-08;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 2 PAYVFEKEDFLDGDG 15

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GenCore version 5.1.4\_P5\_4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 10.1433 Seconds  
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Title: US-09-807-148-4

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Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	11	6.1	12	1	US-08-045-261-1
4	11	6.1	12	1	US-08-045-261-4
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6	10	5.6	12	1	US-08-045-261-5
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8	9	5.0	12	1	US-08-045-261-5
9	9	5.0	12	1	US-08-045-261-6
10	9	3.9	410	1	US-08-471-033-40
11	9	3.9	410	1	US-08-471-033-43
12	9	3.9	410	2	US-08-471-044-40
13	9	3.9	410	2	US-08-471-044-43
14	9	3.9	410	2	US-08-463-483A-40
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20	9	3.9	410	2	US-08-469-334-40
21	9	3.9	410	2	US-08-469-334-43
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23	9	3.9	410	3	US-09-300-529-43
24	9	3.9	446	4	US-08-960-780-52
25	9	3.9	449	1	US-09-073-898-52
26	9	3.9	449	2	US-08-471-033-46
27	9	3.9	449	2	US-08-471-044-46
					Sequence 46, Appl

28	7	3.9	449	2	US-08-471-046A-46	Sequence 46, Appl
29	7	3.9	449	2	US-08-470-566B-46	Sequence 46, Appl
30	7	3.9	449	3	US-08-469-334-46	Sequence 46, Appl
31	7	3.9	449	3	US-09-300-529-46	Sequence 46, Appl
32	7	3.9	462	1	US-08-471-033-2	Sequence 2, Appl1
33	7	3.9	462	1	US-08-471-033-2	Sequence 2, Appl1
34	7	3.9	462	2	US-08-463-483A-2	Sequence 2, Appl1
35	7	3.9	462	2	US-08-471-046A-2	Sequence 2, Appl1
36	7	3.9	462	2	US-08-470-566B-2	Sequence 2, Appl1
37	7	3.9	462	2	US-08-469-334-2	Sequence 2, Appl1
38	7	3.9	462	3	US-09-300-529-2	Sequence 2, Appl1
39	7	3.9	593	1	US-08-296-362-2	Sequence 2, Appl1
40	7	3.9	1009	4	US-09-693-146-4	Sequence 2, Appl1
41	7	3.9	1338	1	US-08-471-033-50	Sequence 50, Appl
42	7	3.9	1338	2	US-08-471-044-50	Sequence 50, Appl
43	7	3.9	1338	2	US-08-463-483A-50	Sequence 50, Appl
44	7	3.9	1338	2	US-08-471-046A-50	Sequence 50, Appl
45	7	3.9	1338	2	US-08-470-566B-50	Sequence 50, Appl

## ALIGNMENTS

RESULT 1  
US-08-946-026-53  
; Sequence 53, Application US/08946026  
; Patent No. 6034218  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Dillon, David C.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Mitcham, Jennifer L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/946,026  
FILING DATE: 07-OCT-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Markl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.424C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-946-026-53  
Query Match 7.8%; Score 14; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.3e-08;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 2 PAYVFKEDFLDGDG 15  
DB 2 PAYVFKEDFLDGDG 15

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OW protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 10.1433 Seconds  
(without alignments)  
522.132 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180

Sequence: 1 EPAYVFEKQFLDGDGWTSRW.....PDNTYEVKIDNSQVSGSLE 180

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCtus.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	12	6.7	12	1	US-08-045-261-2
3	11	6.1	12	1	US-08-045-261-1
4	11	6.1	12	1	US-08-045-261-4
5	10	5.6	12	1	US-08-045-261-3
6	10	5.6	12	1	US-08-045-261-5
7	10	5.6	12	1	US-08-045-261-6
8	9	5.0	12	1	US-08-675-816-2
9	9	3.9	410	1	US-08-471-033-40
10	7	3.9	410	1	US-08-471-033-43
11	7	3.9	410	2	US-08-471-044-40
12	7	3.9	410	2	US-08-471-044-43
13	7	3.9	410	2	US-08-463-483A-40
14	7	3.9	410	2	US-08-463-483A-43
15	7	3.9	410	2	US-08-471-046A-40
16	7	3.9	410	2	US-08-471-046A-43
17	7	3.9	410	2	US-08-470-566B-40
18	7	3.9	410	2	US-08-470-566B-43
19	7	3.9	410	2	US-08-469-334-40
20	7	3.9	410	2	US-08-469-334-43
21	7	3.9	410	3	US-09-300-529-40
22	7	3.9	410	3	US-09-300-529-43
23	7	3.9	446	4	US-08-960-780-52
24	7	3.9	446	4	US-09-073-898-52
25	7	3.9	449	1	US-08-471-033-46
26	7	3.9	449	2	US-08-471-044-46
27	7	3.9	449	2	US-08-463-483A-46

28	7	3.9	449	2	US-08-471-046A-46	Sequence 46, Appl
29	7	3.9	449	2	US-08-470-566B-46	Sequence 46, Appl
30	7	3.9	449	2	US-08-469-334-46	Sequence 46, Appl
31	7	3.9	449	3	US-09-300-529-46	Sequence 46, Appl
32	7	3.9	462	1	US-08-471-033-46	Sequence 2, Appl1
33	7	3.9	462	2	US-08-471-044-2	Sequence 2, Appl1
34	7	3.9	462	2	US-08-463-483A-2	Sequence 2, Appl1
35	7	3.9	462	2	US-08-471-046A-2	Sequence 2, Appl1
36	7	3.9	462	2	US-08-470-566B-2	Sequence 2, Appl1
37	7	3.9	462	2	US-08-469-334-2	Sequence 2, Appl1
38	7	3.9	462	3	US-09-300-529-2	Sequence 2, Appl1
39	7	3.9	593	1	US-08-296-362-2	Sequence 2, Appl1
40	7	3.9	1009	4	US-09-693-146-4	Sequence 4, Appl1
41	7	3.9	1338	1	US-08-471-033-50	Sequence 50, Appl
42	7	3.9	1338	2	US-08-471-044-50	Sequence 50, Appl
43	7	3.9	1338	2	US-08-463-483A-50	Sequence 50, Appl
44	7	3.9	1338	2	US-08-471-046A-50	Sequence 50, Appl
45	7	3.9	1338	2	US-08-470-566B-50	Sequence 50, Appl

#### ALIGNMENTS

RESULT 1  
US-08-946-026-53  
; Sequence 53, Application US/08946026  
; Patent No. 6034218  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Twardzik, Daniel R.  
; APPLICANT: Mitcham, Jennifer L.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
; TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/946,026  
; FILING DATE: 07-OCT-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Makl, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.424C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-946-026-53  
Query Match 7.8%; Score 14; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.3e-08;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PAVYFEKQFLDGDG 15  
DB 2 PAVYFEKQFLDGDG 15

RESULT 2  
US-08-045-261-2  
; Sequence 2, Application US/08045261  
; Patent No. 5426097  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Kuwabara, Keisuke  
; APPLICANT: Ryan, Jane  
; APPLICANT: Benedict, Claude  
; TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White - Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/045,261  
; FILING DATE: 19930406  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/43104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; TELEX: 422523 COOPUI  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-045-261-2  
Query Match 6.7%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.9e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AVEFKQFLDGD 14  
Db 1 AVEFKQFLDGD 12

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/045,261  
; FILING DATE: 19930406  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/43104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; TELEX: 422523 COOPUI  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-045-261-1  
Query Match 6.1%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.5e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VYFKQFLDGD 14  
Db 2 VYFKQFLDGD 12

RESULT 4  
US-08-045-261-4  
; Sequence 4, Application US/08045261  
; Patent No. 5426097  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Kuwabara, Keisuke  
; APPLICANT: Ryan, Jane  
; APPLICANT: Benedict, Claude  
; TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White - Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/045,261  
; FILING DATE: 19930406  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/43104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; TELEX: 422523 COOPUI  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids



TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-4

Query Match 6.1%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.5e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFKEQFLDGD 14  
|||||  
Db 2 YFKEQFLDGD 12

RESULT 5  
US-08-045-261-3  
Sequence 3, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:  
APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOPU  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-3

Query Match 5.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00092;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YFKEQFLDGD 14  
|||||  
Db 3 YFKEQFLDGD 12

RESULT 6  
US-08-045-261-5  
Sequence 5, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:

APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOPU  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-5

Query Match 5.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00092;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YFKEQFLDGD 14  
|||||  
Db 3 YFKEQFLDGD 12

RESULT 7  
US-08-045-261-6  
Sequence 6, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:  
APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261

FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28, 678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-6

Query Match 5.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00092;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKQFPLDGD 14  
DB 3 YKQFPLDGD 12

RESULT 8  
US-08-675-816-2  
Sequence 2, Application US/08675816  
Patent No. 6171864  
GENERAL INFORMATION:  
APPLICANT: Coughlan, Sean J.  
APPLICANT: Manfrey, Jr., Ron J.  
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 701 Fifth Ave. Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675, 816  
FILING DATE: 05-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6171864tendburg, Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 750027.401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206-622-4900  
TELEFAX: (206)-682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-675-816-2

Query Match 5.0%; Score 9; DB 4; Length 415;  
Best Local Similarity 100.0%; Pred. No. 0.26;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMGPD1G 121

DB 131 IMGPD1G 139

RESULT 9  
US-08-471-033-40  
Sequence 40, Application US/08471033  
Patent No. 5770696  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory W  
APPLICANT: Koziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,033  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: P-40,403  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-033-40

Query Match 3.9%; Score 7; DB 1; Length 410;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKQFPLD 12  
DB 121 FKQFPLD 127

RESULT 10  
US-08-471-033-43  
Sequence 43, Application US/08471033  
Patent No. 5770696

GENERAL INFORMATION:  
APPLICANT: Warren, Gregory M  
APPLICANT: Kozziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,033  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: P-40,403  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-033-43

Query Match 3.9%; Score 7; DB 1; Length 410;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FREQFLD 12  
Db 121 FREQFLD 127

RESULT 11  
US-08-471-044-40  
Sequence 40, Application US/08471044  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory M  
APPLICANT: Kozziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy

APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,044  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/463,483  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40,403  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-044-40

Query Match 3.9%; Score 7; DB 2; Length 410;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FREQFLD 12  
Db 121 FREQFLD 127

RESULT 12  
US-08-471-044-43  
Sequence 43, Application US/08471044  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory M  
APPLICANT: Kozziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:

ADDRESSER: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,044  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/463,483  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40,403  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-044-43

Query Match 3.9%; Score 7; DB 2; Length 410;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FKEOFLD 12  
Db 121 FKEOFLD 127

RESULT 13  
US-08-463-483A-40  
Sequence 40, Application US/08463483A  
Patent No. 5849870  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory W  
APPLICANT: Koziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5849870e1 Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA

ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,483A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprull, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8615  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-483A-40

Query Match 3.9%; Score 7; DB 2; Length 410;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FKEOFLD 12  
Db 121 FKEOFLD 127

RESULT 14  
US-08-463-483A-43  
Sequence 43, Application US/08463483A  
Patent No. 5849870  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory W  
APPLICANT: Koziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5849870e1 Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,483A

FILED DATE: 09-SEP-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8615  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-483A-43

Query Match 3.9%; Score 7; DB 2; Length 410;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKEQFLD 12  
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DB 121 FKEQFLD 127

RESULT 15  
US-08-471-046A-40  
Sequence 40, Application US/08471046A  
Patent No. 5866326  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory W  
APPLICANT: Koziele, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal  
TITLE OF INVENTION: Protein Genes  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5866326artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,046A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/463,483  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594

FILED DATE: 09-SEP-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SOLV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-046A-40

Query Match 3.9%; Score 7; DB 2; Length 410;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKEQFLD 12  
|||||  
DB 121 FKEQFLD 127

Search completed: March 14, 2003, 20:50:06  
Job time: 11.1433 secs

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GenCore version 5.1.4\_p5\_4578  
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# OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 70.894 Seconds  
(without alignments)  
783.783 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 417  
Sequence: 1 MLTSLVLLGLGLANVAEPA.....EEDKEDDEEDVFGQAKDEL 417

## Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

## Database :

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	417	100.0	417 10 AAP92276	60 kD Ro (Ro/SSA)
2	417	100.0	417 21 AA92349	Human MBP-calretic
3	417	100.0	417 23 AAE24591	Human calreticulin
4	417	100.0	417 23 AAU77712	Human calreticulin
5	417	100.0	417 23 AAE18851	Human calreticulin
6	400	95.9	400 21 AA92350	Recombinant human
7	382	91.6	417 20 AA900927	Calreticulin. Hom
8	280	67.1	280 21 AA92355	Recombinant delta-
9	180	43.2	180 21 AA92351	Human vasalectin (
10	124	29.7	401 18 AAW1156	Calreticulin. Hom

11	122	29.3	122	20	AA900924	Human cC1qR bindin
12	113	27.1	177	23	ABP42414	Human ovarian anti
13	69	16.5	122	20	AA900925	Mouse cC1qR bindin
14	69	16.5	122	20	AA900926	Rat cC1qR binding
15	67	16.1	70	21	AA844058	Human cancer assoc
16	61	14.6	61	21	AA92352	Recombinant human
17	60	14.4	60	21	AA92354	Recombinant human
18	49	11.8	49	21	AA92353	Recombinant human
19	24	5.8	57	21	AA92422	Human secreted pro
20	19	4.6	19	18	AAW24919	Anti-Ro/SSA antibo
21	19	4.6	336	12	AAW12312	Partial sequence o
22	19	4.6	406	22	AB864414	Drosophila melanog
23	17	4.1	403	17	AAW4171	Flea calreticulin
24	16	3.8	85	17	AAW4170	Flea calreticulin
25	15	3.6	15	19	AAW76256	Human calreticulin
26	15	3.6	15	19	AAW54561	Peptide from Calre
27	15	3.6	18	22	AA898994	N-terminal calretic
28	14	3.4	14	19	AAW76270	Human calreticulin
29	14	3.4	15	18	AAW73317	Alpha-human fructo
30	14	3.4	15	20	AAW02460	Fragment of human
31	13	3.1	13	23	AAE18844	Human calreticulin
32	13	3.1	13	23	AAE18845	Human calreticulin
33	13	3.1	13	23	AAE18846	Human calreticulin
34	13	3.1	415	22	AA866341	Castor bean calret
35	13	3.1	415	22	AA866343	Castor bean calret
36	13	3.1	420	23	AB804656	Maize calreticulin
37	12	2.9	12	19	AAW76267	Human calreticulin
38	12	2.9	12	19	AAW76268	Human calreticulin
39	12	2.9	12	23	AAE18840	Human calreticulin
40	11	2.6	11	19	AAW76266	Human calreticulin
41	11	2.6	11	19	AAW76269	Human calreticulin
42	11	2.6	11	23	AAE18842	Human calreticulin
43	11	2.6	11	23	AAE18843	Human calreticulin
44	11	2.6	16	21	AA923254	Signal peptide use
45	11	2.6	18	19	AAW71681	Endoplasmic reticu

## ALIGNMENTS

RESULT 1  
ID AAP92276 standard; protein: 417 AA.  
XX AAP92276;  
AC  
XX 23-FEB-1990 (first entry)  
DT  
XX 60 kD Ro (Ro/SSA) antigen.  
DE  
XX Sjorens syndrome; systemic lupus erythematosus.  
KW  
XX Synthetic.  
OS  
XX W08909273-A.  
FN  
XX 05-OCT-1989.  
PD  
XX 22-MAR-1989; 89WO-US01213.  
PE  
XX 22-MAR-1988; 88US-0171634.  
PR  
XX (TEXA ) UNIV OF TEXAS SYST.  
PA  
XX Southamer RD, Capra JD, McCauliffe DP;  
PI WPI: 1989-309537/42.  
DR N-PSDB; AAP92276.  
XX  
XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen  
PT - used in immunoassays to detect rheumatic disease  
XX  
XX Disclosure; Fig 2; 88pp; English.  
PS

XX Synthetic peptides corresp. to an epitopic core of Ro antigen are  
CC expressed recombinantly to detect autoantibodies, for identification  
CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,  
CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
CC antigens.

**SQ Sequence 417 AA;**

Query Match	100.0%;	Score 417;	DB 10;	Length 417;
Best Local Similarity	100.0%;	Pred. Nc. 0;		
Matches 417;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	1	M L S V P L L I G L G L A V A E P A Y F R K E O R L D D G M T S R I E S K H N S D E K F V L S S G K F P G D E	60
D b	1	M L S V P L L I G L G L A V A E P A Y F R K E O R L D D G M T S R I E S K H N S D E K F V L S S G K F P G D E	60
OY	61	E K D K G L O T S O D A R E Y A L S A S E P P S N K G O T L V U Q F T W K B H O N I D C G G Y K L P E P N S L D O T	120
D b	61	E K D K G L O T S O D A R E Y A L S A S E P P S N K G O T L V U Q F T W K B H O N I D C G G Y K L P E P N S L D O T	120
OY	121	D M H D S E Y N I M F G D I C G P G T K K V H V I F N T K G K N V L I N K O I R C K D E F T H L Y T L I Y A R P D N	180
D b	121	D M H D S E Y N I M F G D I C G P G T K K V H V I F N T K G K N V L I N K O I R C K D E F T H L Y T L I Y A R P D N	180
OY	181	T Y E Y K I N D S O V E S S L E D M O F L P P K I K I O P D A S K P E D M D E R A K I D P P T O S K R E D M O K P E	240
D b	181	T Y E Y K I N D S O V E S S L E D M O F L P P K I K I O P D A S K P E D M D E R A K I D P P T O S K R E D M O K P E	240
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OY	301	P D P S I Y A I D N F G V I G L D I M O Y K S T I F D N F L I T N D E A Y A E F G N E T W G V T K A A E K O K M K D	360
D b	301	P D P S I Y A I D N F G V I G L D I M O Y K S T I F D N F L I T N D E A Y A E F G N E T W G V T K A A E K O K M K D	360
OY	361	O D E O R L K E E E D K R K E E E A E J K E D D E K D C D E E E E E E K E E E E E D V G O A K M D E L	417
D b	361	O D E O R L K E E E D K R K E E E A E J K E D D E K D C D E E E E E E K E E E E E D V G O A K M D E L	417

RESULT 2	
AAV92349	
ID AAV92349	standard; Protein; 417 AA

AC AAY92349;

DT 10-AUG-2000 (first entry)

Human MBP-calreticulin.

KM MRP-callicuticulin; maltose binding protein; angiogenesis; inhibition;  
KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KM cytosolic; demagogical; immunosuppressive; antiinflammatory; hepatic;  
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

FH	Key	Location/Qualifiers
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5	5	5
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FT	/label= signal_peptide
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F <sup>T</sup>	/label = mature_protein
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100	1

PN W02000020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23240.

PR 06-OCT-1998; 98US-0103438.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

[illegible]

PT useful for suppressing tumor growth

PS Disclosure; Page 79-80; 99pp; English.

CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calcitriol (or its fragments/variants).  
CC Fragments of calcitriol causes at least 40% inhibition of angiogenesis  
CC tumor growth and/or endothelial cell growth (claimed). The method may  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia  
CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Gout/pseudogout's syndrome, systemic vasculitis, scleroderma, Sjögren's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

SQ Sequence 417 AA;

Query Match	100.0%;	Score 417;	DB 21;	Length 417;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 417; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	MLLSVPLLLGLLGLAVAEPAVYFEQFIDGQGMTSMTIESHKHSDPKFVYLSCKFFGDE	60
Db	1	MLLSVPLLLGLLGLAVAEPAVYFEQFIDGQGMTSMTIESHKHSDPKFVYLSCKFFGDE	60
QY	61	EKDKGLQTSODARFVYLSASFEPFSNKGQTLVQFTVKNHEONIDCGGGYKLPFNSLDQT	120
Db	61	EKDKGLQTSODARFVYLSASFEPFSNKGQTLVQFTVKNHEONIDCGGGYKLPFNSLDQT	120
QY	121	DMHDDSENNIMEGDDICGPGTKKHNVLFNKKGKVVLLNKDRCDDDEFTHLYTLVAPDN	180
Db	121	DMHDDSENNIMEGDDICGPGTKKHNVLFNKKGKVVLLNKDRCDDDEFTHLYTLVAPDN	180
QY	181	TYEAKINDSQVESGLIEDDMFLPPKKIKDPDASKPEDMDERAKIDTPTSKPEDMOKPE	240
Db	181	TYEAKINDSQVESGLIEDDMFLPPKKIKDPDASKPEDMDERAKIDTPTSKPEDMOKPE	240
QY	241	HIIPDDAKKPEDMDMEMDGEMEPVIONPEYKGEMKPRQIDNPDKGTWIIHPEIDNPEYS	300
Db	241	HIIPDDAKKPEDMDMEMDGEMEPVIONPEYKGEMKPRQIDNPDKGTWIIHPEIDNPEYS	300
QY	301	PDPBSIYADNNGVGLDLMQYKSGTITDNLITLDEAYAEFGEMTGVYKKAARKOKKD	360
Db	301	PDPBSIYADNNGVGLDLMQYKSGTITDNLITLDEAYAEFGEMTGVYKKAARKOKKD	360
QY	361	QDEBQRLLKEEEDKKRKEEFAEKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE	417
Db	361	QDEBQRLLKEEEDKKRKEEFAEKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE	417
QY	417	QDEBQRLLKEEEDKKRKEEFAEKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE	417
Db	417	QDEBQRLLKEEEDKKRKEEFAEKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE	417

### RESULT 3

ID AAE24591 standard; Protein; 417 AA

AC AAE24591;

DT 04-OCT-2002 (first entry)

DE Human calreticulin protein.



XX	Human; calcitriecin; antisense compound; hyperproliferative disorder;
KM	cancer; autoimmune disease; viral infection; cardiovascular disease;
KW	antisense therapy; cytostatic; immunosuppressive; virucide.
XX	
OS	Homo sapiens.
PN	WO200236743-A2.
XX	
PD	10-MAY-2002.
XX	
PF	30-OCT-2001; 2001WO-US49045.
XX	
PR	30-OCT-2000; 2000US-0702327.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Bennett CF, Cowse LM;
XX	
DR	WPL: 2002-479759/51.
DR	N-PsDB: AAD39469.
XX	
PT	Noval antisense compound targeted to nucleic acid encoding
PT	calcitriecin, useful for treating a human having disease or condition
PT	associated with calcitriecin e.g. cancer, viral infection, autoimmune
PT	disease -
XX	
PS	Disclosure; Page 88-90; 109pp; English.
XX	
CC	The invention relates to antisense compounds, compositions and methods
CC	for modulating the expression of calcitriecin. The compositions comprise
CC	antisense compounds, particularly antisense oligonucleotides, targeted
CC	to nucleic acids encoding calcitriecin. The antisense compound is useful
CC	for inhibiting the expression of calcitriecin in human cells or tissues.
CC	It is also useful for treating a human having a disease or condition
CC	associated with calcitriecin, e.g., hyperproliferative disorder e.g.
CC	cancer, autoimmune disease, viral infection or cardiovascular disease,
CC	by inhibiting expression of calcitriecin. It is useful for diagnostics,
CC	therapeutics, prophylaxis and as research reagents and kits. It is also
CC	used in antisense therapy. The present sequence is human calcitriecin
CC	protein. This sequence is used in the exemplification of the invention.
XX	
SQ	Sequence 417 AA:
Query Match	100.0%; Score 417; DB 23; Length 417;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 417; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MLTSPLLGLGLAVAPVYFKEDFLDGGTWISKHKSDGKFLVSSGKFYGD 60
Db	1 MLTSPVLLGLGLLVAEVPVYFKEDFLDGGTWISKHKSDGKFLVSSGKFYGD 60
OY	61 EKDKGLOTQODARFALASPEPFSNKGOTLVVOFVHKEONIDCGGVTKLPNSLDOT 120
Db	61 EKDKGLOTQODARFALASPEPFSNKGOTLVVOFVHKEONIDCGGVTKLPNSLDOT 120
OY	121 DMHGSEVNIMGPDIICGRTKKVHYIFNYKKNVLINDICKODEFHLYTLVLRPN 180
Db	121 DMHGSEVNIMGPDIICGRTKKVHYIFNYKKNVLINDICKODEFHLYTLVLRPN 180
OY	181 TTEVKITDSNVSGSLIEDDDWFLPKKIKDPASKREDEDERAKIDDPTDSKPEDMDKPE 240
Db	181 TTEVKITDSNVSGSLIEDDDWFLPKKIKDPASKREDEDERAKIDDPTDSKPEDMDKPE 240
OY	241 HTPDDAKRPEWDEMOGEWPVIQNFEYGEKMPRIIDNPDKGTIIHEINDPEPS 300
Db	241 HTPDDAKRPEWDEMOGEWPVIQNFEYGEKMPRIIDNPDKGTIIHEINDPEPS 300
OY	301 PDPSTIAYDNFCVLIDLTVQVKSGLTFDNFLTNDENAYKEEFNGNETWGVTKAEEKOMKDK 360
Db	301 PDPSTIAYDNFCVLIDLTVQVKSGLTFDNFLTNDENAYKEEFNGNETWGVTKAEEKOMKDK 360
OY	361 ODEQRRLKEEEEDKKRKEEAEKDEDEDKDEDEDEDEDEDEDEDEDEVDVGQAQDEL 417

ID	Query Match	Best Local Similarity	Matches 417: Conservative	Score 417: 100.0%	DB 23: Pred. No. 0;	Length 417: 0;	Mismatches 0;	Indels 0;	Gaps 0;
XX	AAU77712	AAU77712 standard; Protein; 417 AA.							
XX	AAU77712	05-JUN-2002 (first entry)							
XX	AAU77712	Human calreticulin (CRT).							
XX	AAU77712	Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;							
XX	AAU77712	cytotoxic; vaccine; human Papillomavirus 16; HPV 16; E7; DNA vaccine;							
XX	AAU77712	enhanced antigen-specific immune response; cytotoxic T lymphocyte;							
XX	AAU77712	tumour; cancer; cervical cancer.							
XX	AAU77712	Homo sapiens.							
XX	AAU77712	WO200212281-A2.							
XX	AAU77712	14-FEB-2002.							
XX	AAU77712	02-AUG-2001; 2001WO-US24134.							
XX	AAU77712	03-AUG-2000; 2000US-222902P.							
XX	AAU77712	(UYJO ) UNIV JOHNS HOPKINS.							
XX	AAU77712	Wu T, Hung C;							
XX	AAU77712	WPI: 2002-257463/30.							
XX	AAU77712	N-PSDB; ABK11662.							
XX	AAU77712	New nucleic acids encoding a fusion polypeptide comprising an							
XX	AAU77712	endoplasmic reticulum chaperone polypeptide linked to an antigenic							
XX	AAU77712	polypeptide, useful as a vaccine for inducing antigen-specific immune							
XX	AAU77712	responses							
XX	AAU77712	Disclosure: Page 27; 71pp; English.							
XX	AAU77712	The invention describes a nucleic acid molecule (1) encoding a fusion							
XX	AAU77712	polypeptide comprising a first polypeptide domain comprising an							
XX	AAU77712	endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and							
XX	AAU77712	a second polypeptide domain comprising at least one antigenic peptide							
XX	AAU77712	e.g. Human Papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as							
XX	AAU77712	a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune							
XX	AAU77712	responses, particularly those mediated by cytotoxic T lymphocytes. The							
XX	AAU77712	nucleic acid and compositions comprising the nucleic acid is also useful							
XX	AAU77712	for inhibiting the growth of tumours and cancers e.g. cervical cancer.							
XX	AAU77712	This is the amino acid sequence of the human calreticulin (CRT), an							
XX	AAU77712	endoplasmic reticulum protein used in the creation of a DNA vaccine.							
XX	AAU77712	Sequence 417 AA:							
XX	AAU77712	Query Match							
XX	AAU77712	Best Local Similarity 100.0%; Score 417: DB 23; Length 417:							
XX	AAU77712	Matches 417: Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
XX	AAU77712	1 MLTSLPRLILGLLGLAVAEPAVYFKKQFLDGDGMTSRMIESKHKSDFGKFLVSSGKRYGDE 60							
XX	AAU77712	1 MLTSLPRLILGLLGLAVAEPAVYFKKQFLDGDGMTSRMIESKHKSDFGKFLVSSGKRYGDE 60							
XX	AAU77712	61 EKDKGLOTSDARFAYALSASFEPSSNKGGTLLVVOFTVYKHEQNIIDCGGCVKLFPSLDT 120							
XX	AAU77712	61 EKDKGLOTSDARFAYALSASFEPSSNKGGTLLVVOFTVYKHEQNIIDCGGCVKLFPSLDT 120							
XX	AAU77712	121 DMHGSSEVNIIMGPRDLCGGTAKVNIIFNYKKANLKNIDCKKDFTHLTLLVLRPN 180							
XX	AAU77712	121 DMHGSSEVNIIMGPRDLCGGTAKVNIIFNYKKANLKNIDCKKDFTHLTLLVLRPN 180							



PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Tosato G, Pike SE, Yao L:  
XX WPI: 2000-303767/26.  
DR N-PSDB: AAA09346, AAA09347.  
XX  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
XX  
XX Claim 4: Page 80-81; 99pp; English.  
XX  
XX Recombinant human MBP-calreticulin comprises the sequence of human  
CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
CC A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of  
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
CC method may be used for inhibiting angiogenesis in a patient. The  
CC angiogenesis is associated with a disease other than a tumor that is  
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodromas,  
CC Immune inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).  
XX  
XX Sequence 400 AA:  
SQ  
Query Match 95.9%; Score 400; DB 21; Length 400;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 18 EPAYFKRQPLDGGDWTSRWIESKHKSDPGKFLVSSGKFGDEKDKGLQTSODARFYAL 77  
Db 1 EPAYFKRQPLDGGDWTSRWIESKHKSDPGKFLVSSGKFGDEKDKGLQTSODARFYAL 60  
QY 78 SASPEPFSNKGQTLVQFTVKHEQNDICGGGVYKLFPSNLDQTMHGSEYVIMFGPDLIC 137  
Db 61 SASPEPFSNKGQTLVQFTVKHEQNDICGGGVYKLFPSNLDQTMHGSEYVIMFGPDLIC 120  
QY 138 GPGTKKVVHIFNYKGNVLINKDIRCKDEFTHLTYTLVPRDNTYEVKIDNSQVESGSL 197  
Db 121 GPGTKKVVHIFNYKGNVLINKDIRCKDEFTHLTYTLVPRDNTYEVKIDNSQVESGSL 180  
QY 198 DDMWDLPPKTKIRDPDASKPEMDERAKIDDPDTSKPEMDKREHLPDPDAKPEMDDEEM 257  
Db 191 DDMWDLPPKTKIRDPDASKPEMDERAKIDDPDTSKPEMDKREHLPDPDAKPEMDDEEM 240  
QY 258 DGEWPEPVYIONPEYKGEKMPROIDNPDKGTWIHPEIDNPEYSPDPSIAYNFGVLGD 317  
Db 241 DGEWPEPVYIONPEYKGEKMPROIDNPDKGTWIHPEIDNPEYSPDPSIAYNFGVLGD 300  
QY 318 LMQVSGTIFDNFLITNDPAVAEEFGNETWGTAKAEKOMDKODEBQRLKEEEDKKRK 377  
Db 301 LMQVSGTIFDNFLITNDPAVAEEFGNETWGTAKAEKOMDKODEBQRLKEEEDKKRK 360  
QY 378 EEEEAEDKEDDEDKDE 417  
Db 361 EEEEAEDKEDDEDKDE 400

XX  
DE Calreticulin.  
XX C1q and collectin receptor: c1qg binding domain; complement ubiquitin;  
KW CUB functional; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
OS Homo sapiens.  
XX WO9907406-A1.  
XX 18-FEB-1999.  
XX 12-AUG-1998; 98WO-GB02430.  
XX 12-AUG-1997; 97GB-0016998.  
XX (UYLE-) UNIV LEICESTER.  
XX Schwaebler W;  
DR WPI: 1999-180404/15.  
XX  
XX use of a C1qg binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
PS Disclosure: Page 26-27; 31pp; English.  
XX  
CC This sequence is calreticulin, a homologue of C1q and collectin receptor  
CC (C1qR). The invention relates to the use of a C1qg binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the C1qg binding domain in a medicament to inhibit CUB  
CC functionality. The C1qg binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of C1qg binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
SQ Sequence 417 AA:  
Query Match 91.6%; Score 382; DB 20; Length 417;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 36 RWIESKHKSDPGKFLVSSGKFGDEKDKGLQTSODARFYALSASPEPFSNKGQTLVQF 95  
Db 36 RWIESKHKSDPGKFLVSSGKFGDEKDKGLQTSODARFYALSASPEPFSNKGQTLVQF 95  
QY 96 TVKHEDNDICGGGVYKLFPSNLDQTMHGSDSEYVIMFGPDLICGPGTKKVVHIFNYKGNV 155  
Db 96 TVKHEDNDICGGGVYKLFPSNLDQTMHGSDSEYVIMFGPDLICGPGTKKVVHIFNYKGNV 155  
QY 156 LINKDIRCKDEFTHLTYTLVPRDNTYEVKIDNSQVESGSLDDMDLPPKTKIRDPDASK 215  
Db 156 LINKDIRCKDEFTHLTYTLVPRDNTYEVKIDNSQVESGSLDDMDLPPKTKIRDPDASK 215  
QY 216 PEDWDERAKIDDPDTSKPEMDKPEHIPPDAKPEMDWDEMDGEWPEPVYIONPEYKGM 275  
Db 216 PEDWDERAKIDDPDTSKPEMDKPEHIPPDAKPEMDWDEMDGEWPEPVYIONPEYKGM 275  
QY 276 KPRQIDNPDKGTWIHPEIDNPEYSPDPSIAYNFGVLGLDMQVSGTIFDNFLITND 335  
Db 276 KPRQIDNPDKGTWIHPEIDNPEYSPDPSIAYNFGVLGLDMQVSGTIFDNFLITND 335  
QY 336 EAYAEFGNETWGTAKAEKOMDKODEBQRLKEEEDKKRKEEBAEDKEDDEDEDEDEDE 395  
Db 336 EAYAEFGNETWGTAKAEKOMDKODEBQRLKEEEDKKRKEEBAEDKEDDEDEDEDEDE 395

QY	396	EDEEDKEDEEDVPGQAKDEL	417
Db	396	EDEEDKEDEEDVPGQAKDEL	417
RESULT 8			
ID	AA923355		
AC	AA923355 standard; Protein; 280 AA.		
XX	AA923355;		
XX	10-AUG-2000 (first entry)		
DE	Recombinant delta-120 calcitriol.		
XX			
KM	MBP-calcitriol; maltose binding protein; angiogenesis; inhibition;		
KM	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;		
KM	cytotoxic; dermatological; immunosuppressive; antiinflammatory; hepatic;		
XX	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.		
XX			
OS	Homo sapiens.		
XX	Synthetic.		
PN	WO200020577-A1.		
PD	13-APR-2000.		
XX			
PE	05-OCT-1999; 99WO-US23240.		
XX			
PR	06-OCT-1998; 98US-0103438.		
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.		
PI	Tosato G, Pike SE, Yao L.		
XX	WPI: 2000-303767/26.		
PT	Inhibiting endothelial cell growth and angiogenesis using calcitriol,		
XX	useful for suppressing tumor growth		
PS	Claim 4; Page 86; 99pp; English.		
XX			
CC	This sequence comprises recombinant human calcitriol (AA923350)		
CC	missing the N-terminal 120 amino acids.		
CC	A novel method of inhibiting endothelial cell growth comprises		
CC	contacting the cells with calcitriol (or its fragments/variants).		
CC	Fragments of calcitriol causes at least 40% inhibition of		
CC	angiogenesis, tumor growth and/or endothelial cell growth (claimed). The		
CC	method may be used for inhibiting angiogenesis in a patient. The		
CC	angiogenesis is associated with a disease other than a tumor that is		
CC	associated with neovascularization (e.g. diabetic neuropathy, retrolental		
CC	fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas,		
CC	immune inflammation, atherosclerosis, excessive wound repair, retinal		
CC	neovascularization, macular degeneration, corneal graft rejection,		
CC	contact lens overwear, Crohn's disease, non-immune inflammation,		
CC	rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,		
CC	Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's		
CC	syndrome, sarcoidosis and primary biliary cirrhosis). The method may		
CC	also be used for treating/inhibiting tumor growth especially		
CC	Kaposi's sarcoma (claimed).		
XX			
XX			
Sequence	280 AA;		
Query Match	67.1%; Score 280; DB 21; Length 280;		
Best Local Similarity	100.0%; Pred. No. 6.9e-267;		
Matches	280; Conservative 0; Mismatches 0; Indels 0; Gaps 0.		
QY	138	GGTGGVAVIENFKGNVLIINKDICKDEFTLTLIVRPDNTFEVKIDNSQVESGSL	197
Db	1	GGTGGVAVIENFKGNVLIINKDICKDEFTLTLIVRPDNTFEVKIDNSQVESGSL	60
QY	198	DDWDFLPKKIKDPDASKPEMDERAKIDDPDTSKPEMDKDEHILPDPDAKPEMDDEEM	257

Db	61	DDMDFLPKRIKDDPDAKSPEDMDERAKIDDPDTSKREDDMDKREHILPDDPAKKPEDDWDEM	120
Qy	258	DGEWEPYIQNPEKKGWKRQIDNDPYKKTWTHPEIDNPEYSPDPSIYADNFGVLGD	317
Db	121	DGEWEPYIQNPEKKGWKRQIDNDPYKKTWTHPEIDNPEYSPDPSIYADNFGVLGD	180
Qy	318	LMQVKSSTIFNFIITNDEAYAEFEFGNEMTWGVTAKAEKQMKRKODEQRKKEEEDKRRK	377
Db	181	LMQVKSSTIFNFIITNDEAYAEFEFGNEMTWGVTAKAEKQMKRKODEQRKKEEEDKRRK	240
Qy	378	EEEEAEDEKDEDEKDEDEDEDEKDEDEEDYVGAQKDEL	417
Db	241	EEEEAEDEKDEDEKDEDEDEDEKDEDEEDYVGAQKDEL	280
RESULT 9			
ID	AAV92351	standard; Protein; 180 AA.	
XX	AAV92351:		
XX	AAV92351:		
DT	10-AUG-2000	(first entry)	
DE	Human vasostatin (calreticulin N-terminal 180 amino acids).		
XX			
KW	MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;		
KW	angiogenesis; inhibition; endothelial cell; anti-angiogenic;		
KW	neuroprotective; antidiabetic; cycostatic; dermatological; hepatic;		
KW	immunosuppressive; anti-inflammation; anti-atherosclerotic;		
KW	gastrointestinal; anti-arthritis; ophthalmic.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
XX	MO200020577-A1.		
FN	13-APR-2000.		
PD			
XX	13-APR-2000.		
XX			
PF	05-OCT-1999;	99MO-US23240.	
XX			
PR	06-OCT-1998;	98US-0103438.	
XX			
XX	(USSH ) US DEPT HEALTH & HUMAN SERVICES.		
PA			
XX			
XX	Tosato G, Pike SE, Yao L;		
PI	WPI, 2000-303767/26.		
DR			
XX			
XX			
PS	Claim 4; Page 82; 99pp; English.		
XX			
XX			
CC	A novel method of inhibiting endothelial cell growth comprises		
CC	contacting the cells with calreticulin (or its fragments/variants).		
CC	Fragments of calreticulin causes at least 40% inhibition of angiogenesis,		
CC	tumor growth and/or endothelial cell growth (claimed). The method may be		
CC	used for inhibiting angiogenesis in a patient. The angiogenesis is		
CC	associated with a disease other than a tumor that is associated with		
CC	neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,		
CC	trachoma, neovascular glaucoma, psoriasis, angiodermas, immune		
CC	inflammation, atherosclerosis, excessive wound repair, retinal		
CC	neovascularization, macular degeneration, corneal graft rejection,		
CC	cataract lens overwear, Crohn's disease, non-immune inflammation,		
CC	rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,		
CC	goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's		
CC	syndrome, sarcoidosis and primary biliary cirrhosis). The method may		
CC	also be used for treating/inhibiting tumor growth especially		
CC	Kaposi's sarcoma (claimed).		
XX			
XX			
Sequence	180 AA:		
50			

Query Match	43.2%	Score 180;	DB 21;	Length 180;
Best Local Similarity	100.0%	Pred. No. 1.1e-168;		
Matches 180;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT	10
AAW11156	
ID	AAW11156 standard; peptide: 401 AA.

AC	AAM11156;
XX	
DT	31-MAY-1997 (first entry)
XX	
DE	Calreticulin.
XX	
KW	calreticulin; C-domain; restenosis; inhibitor

OS	Homo sapiens.
XX	
PN	WC9636643-A1.
XX	
PD	21-NOV-1996.
XX	
PF	17-MAY-1996; 96WO-IB00471.
XX	
PR	16-MAY-1996; 96US-0649417.
PR	17-MAY-1995; 95US-0442844.
XX	
PA	(UYAL-) UNIV ALBERTA.
XX	
PI	Lucas A, Michalak M;
XX	
DR	WPI; 1997-012036/01.
XX	
PT	Inhibition of restenosis in patients - using calreticulin or a
PT	C-domain polypeptide of calreticulin or a variant with the same
PT	activity.

PS	Disclosure; Fig 1; 48bp; English.
XX	
CC	The present sequence is calcitriecin. It and a C-domain derived peptide
CC	(AAW06730) are useful for treating a patient to inhibit restenosis. T
CC	calcitricilin-type cpds. are administered either parenterally,
CC	intravenously or via a catheter and can target areas of vascular damaa
CC	to inhibit or prevent restenosis.
XX	
SQ	Sequence      401 AA;
	Query Match            29.7%; Score 124; DB 18; Length 401;
	Best Local Similarity   100.0%; Pred. No. 2.7e-113;
	Matches 124; Conservative   0; Mismatches   0; Indels   0; Gaps
OY	121 DMHDSRYNIMFGPDIGPGCTKKVHFNFKNKKNVLINKDIRCKODEFTILYLIVRPN 180
Dd	104 DMHDSRYNIMFGPDIGPGCTKKVHFNFKNKKNVLINKDIRCKODEFTILYLIVRPN 163
OY	181 TYEYKIDNSOVESGSLDDMDLFLEPPKKIKOPDASKPEDWDERAKIDDPDTSKPEDWDKPE 240
Dd	164 TYEYKIDNSOVESGSLDDMDLFLEPPKKIKOPDASKPEDWDERAKIDDPDTSKPEDWDKPE 223
OY	241 HIPD 244

Db 224 HIPD 227

RESULT 11  
AAY00924  
ID AAY00924 standard; Protein; 122 AA.

AC	AAV00924;	
XX		
DT	28-MAY-1999	(first entry)
XX		
DE	Human cC1qR binding domain protein sequence	

KM C1g and collectin receptor; C1qR binding domain; complement ubiquitin;  
KM C3b functionality; inhibitor; complement activation; inflammation;  
KM myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KM rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KM immune complex nephritis; therapy.

OS Homo sapiens.  
XX  
PN WO9907406-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 12-AUG-1998; 98WO-GB02430.  
XX  
PR 12-AUG-1997; 97GB-0016998.  
XX  
PR  
PA (UYLE-) UNIV LEICESTER.  
XX  
XX  
PI Schwaebler W;  
XX  
DR WPI: 1999-180404/15.  
DR N-PSDB; AAX27251.  
XX  
XX  
PT Use of a cC1qR binding domain - to modulate complement ubiquitination  
PT (CUB) functionality.

	PS	Claim 9, Page 23; 31pp; English.
XX	CC	This sequence is a C1q and collectin receptor (cC1qR) binding domain. The invention relates to the use of a cC1qR binding domain in a medicament to effect complement ubiquitin (CUB) functionality, and an inhibitor of the cC1qR binding domain in a medicament to inhibit CUB functionality. The cC1qR binding domain, or its inhibitor, can be used to treat a human or animal body. Particularly an inhibitor is used to complement activation involved in the initiation and maintenance of inflammation, for example in myocardial infarction, brain ischemia (stroke), gut ischemia, rheumatoid arthritis, systemic lupus erythematosus, burns, immune complex nephritis, and to treat amyloid plaques in Alzheimer's disease. The use of cC1qR binding domain or inhibitor enables the CUB domain functionality to be modulated using a low molecular weight molecule.
XX	Sequence	122 AA;
SQ	Query Match	29.3%; Score 122; DB 20; Length 122; Best Local Similarity 100.0%; Pred. No. 8,5e-112;
	Matches 122:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	Db	162 RCKDDEFHLYTLVLRPNNTYEKIDNSQVESGSLDDMDLPPKKIKDPDAKREDMDE 221           1 RCKDDEFHLYTLVLRPNNTYEKIDNSQVESGSLDDMDLPPKKIKDPDAKREDMDE 60
OY	Db	222 RAKIDDDPTDSKPEDMDKPEHI PDDPAKKRPEDMDDEMDGEWEPVIQNEPYIGGWKPRPID 281           61 RAKIDDDPTDSKPEDMDKPEHIPDDPAKKRPEDMDDEMDGEWEPVIQNEPYIGGWKPRPID 120
OY	Db	282 NP 283 
DB		121 NP 122



Query Match 16.5%; Score 69; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.2e-59;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 KPEMDERAKIDDPDSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 274  
|||||  
DB 54 KPEMDERAKIDDPDSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 113  
|||||

QY 275 WKPROIDNP 283  
|||||  
DB 114 WKPROIDNP 122

RESULT 14  
AA00926  
ID AAY00926 standard; Protein: 122 AA.  
XX  
AC AAY00926;  
XX  
DT 28-MAY-1999 (first entry)  
XX  
DE Rat cC1qR binding domain protein sequence.  
XX  
KW C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;  
KW CUB functional; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
KW  
XX  
OS Rattus norvegicus.  
XX  
PN WO9907406-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 12-AUG-1998; 98WO-GB02430.  
XX  
PR 12-AUG-1997; 97GB-0016998.  
XX  
PA (UTLE-) UNIV LEICESTER.  
XX  
PI Schwaebel W;  
XX  
DR WPI: 1999-180404/15.  
DR N-PSDB: AAX27253.  
XX  
PT Use of a cC1qR binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
XX  
PS Claim 9; Page 24-25; 31pp; English.  
XX  
XX This sequence is a C1q and collectin receptor (cC1qR) binding  
CC domain. The invention relates to the use of a cC1qR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB  
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.  
XX  
SQ Sequence 122 AA;

Query Match 16.5%; Score 69; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.2e-59;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 KPEMDERAKIDDPDSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 274  
|||||

DB 54 KPEMDERAKIDDPDSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 113  
|||||  
QY 275 WKPROIDNP 283  
|||||  
DB 114 WKPROIDNP 122

RESULT 15  
AAB44058  
ID AAB44058 standard; Protein: 70 AA.  
XX  
AC AAB44058;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated protein sequence SEQ ID NO:1503.  
XX  
KW Human; cancer associated gene; cancer antigen; detection; cancer;  
KW diagnosis; cytostatic; proliferative; vulnerability; immunomodulator;  
KW antidiabetic; antisthmatic; antirheumatic; antiarthritic; antiviral;  
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
KW dermatologic; neuroprotective; thrombolytic; coagulant; nootropic;  
KW vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.  
KW  
XX  
OS Homo sapiens.  
XX  
PN WO200055350-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US05882.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI: 2000-587533/55.  
DR N-PSDB: AAC78267.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
PT useful for treating or diagnosing e.g. cancer -  
XX  
PS Claim 11; Page 2179; 2352pp; English.  
XX  
XX AAC7607 to AAC78448 encode the human cancer associated proteins given  
CC in AAB43398 to AAB44233. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnerability; immunomodulator;  
CC antidiabetic; antisthmatic; antirheumatic; antiarthritic;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatologic; neuroprotective; cardiant; thrombolytic; coagulant;  
CC nootropic; vasotropic; antipsoriatic and angiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies and  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 70 AA;

Query Match 16.1%; Score 67; DB 21; Length 70;  
Best Local Similarity 100.0%; Pred. No. 6.4e-58;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 GVLGDLMOVKSGTTFDNLITNDEAYAEFGNENETWGTAKAEKOMKODEORLKEEE 371  
|||||  
Db 2 GVLGDLMOVKSGTTFDNLITNDEAYAEFGNENETWGTAKAEKOMKODEORLKEEE 61

QY 372 EDKRRKE 378  
|||||  
Db 62 EDKRRKE 68

Search completed: March 14, 2003, 20:44:15  
Job time : 72.894 secs

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 55.7593 Seconds  
(without alignments)  
1540.938 Million cell updates/sec

Title: US-09-807-148-2  
Perfect score: 417  
Sequence: 1 MLTSVPLILGLGLAVAEPA.....EDKEDDEEDVFGQAKDEL 417

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SPREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	14.9	417	6	Q8SQ53
2	39	9.4	411	13	Q91710
3	32	7.7	214	4	Q9UDG2
4	30	7.2	321	13	Q9USG0
5	27	6.5	405	5	Q26268
6	27	6.5	421	5	Q9U6S0
7	25	6.0	318	13	Q9PTX7
8	24	5.8	410	5	Q16893
9	23	5.5	375	5	Q18478
10	22	5.3	387	5	Q97372
11	22	5.3	343	13	Q91711
12	22	5.3	417	13	Q9PUC1
13	21	5.0	406	5	Q8WR36
14	20	4.8	395	5	Q96722
15	20	4.8	419	13	Q98984
16	19	4.6	397	5	Q8WPG8

17	19	4.6	403	5	Q76961	Q76961 necator ame
18	19	4.6	406	5	Q9U916	Q9U916 drosophila
19	18	4.3	68	6	Q9TS71	Q9TS71 macaca mula
20	18	4.3	407	5	Q8TP93	Q8TP93 aedes aegyp
21	17	4.1	415	5	Q8WRU9	Q8WRU9 meloidogyne
22	13	3.1	178	11	Q62041	Q62041 mus musculu
23	13	3.1	321	10	Q41799	Q41799 zea mays (m
24	13	3.1	421	10	Q43712	Q43712 zea mays (m
25	12	2.9	350	5	Q26514	Q26514 schistosoma
26	12	2.9	396	5	Q45034	Q45034 schistosoma
27	12	2.9	559	5	Q9NG26	Q9NG26 tritichomo
28	11	2.6	380	11	Q9D9Q6	Q9D9Q6 mus musculu
29	11	2.6	384	4	Q96LN3	Q96LN3 homo sapien
30	11	2.6	384	4	Q96LN2	Q96LN2 homo sapien
31	11	2.6	389	10	Q40567	Q40567 nicotiana t
32	11	2.6	412	10	Q40040	Q40040 hordum vul
33	11	2.6	415	10	Q40041	Q40041 hordum vul
34	11	2.6	422	10	Q22502	Q22502 brassica na
35	11	2.6	428	10	Q41798	Q41798 zea mays (m
36	11	2.6	532	10	Q9LY26	Q9LY26 arabidopsis
37	10	2.4	17	11	Q9QV75	Q9QV75 rattus sp.
38	10	2.4	132	16	Q9RXV0	Q9RXV0 delinococcus
39	10	2.4	536	5	Q95PU5	Q95PU5 dictyostell
40	10	2.4	774	11	Q8RIQ5	Q8RIQ5 mus musculu
41	10	2.4	775	11	Q9D6C5	Q9D6C5 mus musculu
42	10	2.4	775	11	Q9D680	Q9D680 mus musculu
43	9	2.2	70	10	Q9SXW3	Q9SXW3 lithospermu
44	9	2.2	77	16	Q8TP97	Q8TP97 anabena sp
45	9	2.2	101	10	Q40751	Q40751 parthenium

ALIGNMENTS

RESULT 1	ID	Q8SQ53	PRELIMINARY:	PRT:	417 AA.
AC	Q8SQ53:	01-JUN-2002 (TRENBLREL. 21, Created)			
DT	01-JUN-2002 (TRENBLREL. 21, Last sequence update)				
DT	01-JUN-2002 (TRENBLREL. 21, Last annotation update)				
DE	Calreticulin.				
GN	CRT.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OX	Bovidae; Bovinae; Bos.				
RN	NCBI_TaxID=9913;				
RP	SEQUENCE FROM N.A.				
RA	Hossain M.A., Takawa K., Minakata H., Nakajima T.;				
RT	"Bovine brain calreticulin."				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB067687; BAB86913.1;				
SO	SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;				
Query Match	14.9%;	Score 62;	DB 6;	Length 417;	
Best Local Similarity	100.0%;	Pred. No. 1.2e-54;			
Matches 62;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	117	LDQTMHGDSEYNIWEGPDICGPGTKVHVIFNYGKVVLLNKDIRCKDDERTHLTYLLIV	176		
DB	117	LDQTMHGDSEYNIWEGPDICGPGTKVHVIFNYGKVVLLNKDIRCKDDERTHLTYLLIV	176		
QY	177	RP 178			
DB	177	RP 178			
RESULT 2					
QY	091710				
ID	091710:	PRELIMINARY:	PRT:	411 AA.	
AC	091710:				

```
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS.";
RL Biochem. J. 0:0-0(0).
DR EMBL; X67597; CAA47866.1; -
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 12 POTENTIAL.
FT CHAIN 13 411 CALRETICULIN.
SQ SEQUENCE 411 AA; 48344 MW; 891DA6E0EBEFA CRC64;

Query Match 9.4%; Score 39; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 KPEWDEMDGEMEPVIONPEYKGEKMPROINDPDYKG 287
DB 244 KPEWDEMDGEMEPVIONPEYKGEKMPROINDPDYKG 282

RESULT 3
OY 09UDG2 PRELIMINARY; PRT; 214 AA.
AC 09UDG2.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CALRETICULIN-CALCIUM binding protein (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA Houen G., Koch C.;
RT "Human placental calreticulin: purification, characterization and
RT association with other proteins.";
RL Acta Chem. Scand. 48:905-911(1994).
DR InterPro; IPR001580; Calreticulin.
DR PRODOM; PD001866; Calreticulin.1.
FT NON_TER 1 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 7.7%; Score 32; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.6e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 257 MDGEMEPVIONPEYKGEKMPROINDPDYKGT 288
DB 117 MDGEMEPVIONPEYKGEKMPROINDPDYKGT 148

RESULT 4
OY 09U5G0 PRELIMINARY; PRT; 321 AA.
AC 09U5G0.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Calreticulin (Fragment).
OS Euplatelus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:728-735(1999).
DR EMBL; AB025323; BAA8476.1; -
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AE CRC64;

Query Match 7.2%; Score 30; DB 13; Length 321;
Best Local Similarity 100.0%; Pred. No. 5.8e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 235 DWDKPEHIPDPARKPEMDGEMGEWEP 264
DB 134 DWDKPEHIPDPARKPEMDGEMGEWEP 163

RESULT 5
OY 026268 PRELIMINARY; PRT; 405 AA.
AC 026268.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
CN CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspeidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL; S51239; AAB24569.1; -
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
```

DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 405 AA; 46738 MW; 1ACAA201840D1D69 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 8,4e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 YNMGPDICGPGTKKVVHFNKGN 154  
Db 124 YNMGPDICGPGTKKVVHFNKGN 150

## RESULT 6

OY 090650 PRELIMINARY; PRT; 421 AA.  
AC 090650;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Calreticulin precursor.  
GN CALRET.  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Susan J.M., Just M.L., Lennarz W.J.;  
RT "Cloning and Characterization of Alpha Integrin and Calreticulin in  
RT Embryos of the Sea Urchin."  
RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF177915; AAD55725.1;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; Calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 421 CALRETICULIN.  
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 8,7e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 YNMGPDICGPGTKKVVHFNKGN 154  
Db 127 YNMGPDICGPGTKKVVHFNKGN 153

## RESULT 7

OY 09PTX7 PRELIMINARY; PRT; 318 AA.  
AC 09PTX7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 13, Last annotation update)  
DE Calreticulin (Fragment).  
OS Lehenhleron reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lehenhleron.  
OX NCBI\_TaxID=7753;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=20063780; PubMed=10594174;  
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;

RT "Monophily of lampreys and hagfishes supported by nuclear DNA-coded  
RT genes."  
RL J. Mol. Evol. 49:729-735 (1999).

DR EMBL; AB025328; BAA84841.1;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
FT NON\_TER 1 1  
SQ SEQUENCE 318 AA; 36997 MW; C88102EALICAC1506 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 7,5e-17;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 IMEGPDICGPGTKKVVHFNKGN 154  
Db 29 IMEGPDICGPGTKKVVHFNKGN 53

## RESULT 8

OY 016893 PRELIMINARY; PRT; 410 AA.  
AC 016893;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Calreticulin.  
GN CRT-1.  
OS Amblyomma americanum.  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
OX NCBI\_TaxID=6943;  
RN [1]  
RP SEQUENCE OF 49-410 FROM N.A.  
RC TISSUE-SALIVARY GLANDS;  
RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,  
RA Needham G.R.;  
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
RT saliva."  
RL J. Insect Physiol. 41:369-375 (1995).

RM [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLANDS;  
RA Jaworski D.C.;  
RL Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLANDS;  
RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;  
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; U07708; AAC79694.1;  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00805; CALRETICULIN\_1; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 410 AA; 47485 MW; 32C8B750A17DC54 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 1e-15;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 90 TLVQFTVKNHEQNDICGGGYKLF 113  
Db 89 TLVQFTVKNHEQNDICGGGYKLF 112

```
RESULT 9
ID 018478 PRELIMINARY; PRT: 375 AA.
AC 018478;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RAL-1 protein (Fragment).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA Macleanan K., Hoffman W.H., Taylor D.W.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ001621; CAA04877.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375
SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;
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Query Match 5.5%; Score 23; DB 5; Length 375;  
Best Local Similarity 100.0%; Pred. No. 9.8e-15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 232 KPEDMDKPEHIDPPDAKKPEDMD 254
Db 230 KPEDMDKPEHIDPPDAKKPEDMD 252
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```
RESULT 10
ID 097372 PRELIMINARY; PRT: 387 AA.
AC 097372;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calreticulin precursor.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99094497; PubMed-9879888;
RA Tsui N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.;
RT "Molecular characterization of a calcium-binding protein from the
RT filarial parasite Dirofilaria immitis."
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL; AF052978; AAD03405.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 387 CALRETICULIN.
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;
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Query Match 5.5%; Score 23; DB 5; Length 387;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 232 KPEDMDKPEHIDPPDAKKPEDMD 254
Db 230 KPEDMDKPEHIDPPDAKKPEDMD 252

RESULT 11
ID 091711 PRELIMINARY; PRT: 343 AA.
AC 091711;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS."
RL Biochem. J. 0:0-0(0)
DR EMBL; X67398; CAA47867.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 1
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;
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Query Match 5.3%; Score 22; DB 13; Length 343;  
Best Local Similarity 100.0%; Pred. No. 9.5e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 168 FTHLYTLIVRPDWTVEKIDNS 189
Db 140 FTHLYTLIVRPDWTVEKIDNS 161
```

```
RESULT 12
ID 09PUC1 PRELIMINARY; PRT: 417 AA.
AC 09PUC1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
CN CALR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20190113; PubMed-10660676;
RA Rubinstein A.L., Lee D., Henion P.D., Halpern M.E.;
RT "Genes dependent on zebrafish cyclops function identified by AFRP
RT differential gene expression screen."
RL Genesis 26:86-97(2000).
DR EMBL; AF195882; AAF13700.1; -.
DR ZFIN; ZDB-GENE-000208-17; calr.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
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DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 417 AA; 48723 MW; 2000C5B400469986 CRC64;

Query Match 5.3%; Score 22; DB 13; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 GVLGDLMDQVKSQTIFDNLFT 333  
 Db 312 GVLGDLMDQVKSQTIFDNLFT 333

## RESULT 13

Q8WR36 PRELIMINARY; PRT; 406 AA.  
 AC Q8WR36;  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Calreticulin.  
 OS Anopheles gambiae (African malaria mosquito).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 CC Anophelinae;  
 OC Anophelinae; Anophelinae; Anophelinae;  
 CC NCBI\_TaxID=7165;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Francischelli I.M., Valenzuela J.G., Ribeiro J.M.;  
 RT "Towards a catalog for genes and proteins from the salivary gland of  
 the malaria vector, Anopheles gambiae."  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF457551; AAL68781.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; Calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; UNKNOWN\_1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; UNKNOWN\_1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; UNKNOWN\_3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 406 AA; 46285 MW; 85068B8BCA93931F1 CRC64;

Query Match 5.0%; Score 21; DB 5; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 VESGSLDMDPFLPKKIKDP 211  
 Db 188 VESGSLDMDPFLPKKIKDP 208

## RESULT 14

Q96722 PRELIMINARY; PRT; 395 AA.  
 AC Q96722;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Calcium binding protein calreticulin precursor.  
 OS Taenia solium.  
 CC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
 CC Cyclophyllidae; Taeniidae; Taenia.  
 CC NCBI\_TaxID=6204;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mendlovic F., Ostoa-Saloma P., Flisser A., Laclette J.P.;  
 RT "Molecular characterization of Taenia solium calreticulin."  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF340232; AAK52725.1; -

DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; Calreticulin; 1.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; UNKNOWN\_1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; UNKNOWN\_1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; UNKNOWN\_1.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;

Query Match 4.8%; Score 20; DB 5; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 VOFTVKEHQNIDCGGYVYL 112  
 Db 92 VOFTVKEHQNIDCGGYVYL 111

## RESULT 15

Q98984 PRELIMINARY; PRT; 419 AA.  
 AC Q98984;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Calreticulin.  
 OS Rana rugosa (wrinkled frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 CC NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96387817; PubMed=8654561;  
 RX Yamamoto S., Nakamura M.;  
 RT "Calnexin: its molecular cloning and expression in the liver of the  
 frog, Rana rugosa."  
 RL FEBS Lett. 387:27-32(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96387817; PubMed=8795287;  
 RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;  
 RT "Strong expression of the calreticulin gene in the liver of Rana  
 rugosa tadpoles, but not adult frogs."  
 RL J. Exp. Zool. 275:431-443(1996).  
 DR EMBL: D78589; BA011425.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; Calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; UNKNOWN\_1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 4.8%; Score 20; DB 13; Length 419;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 HLYTLIVRPDMYEVKINDS 189  
 Db 171 HLYTLIVRPDMYEVKINDS 190

Search completed: March 14, 2003, 20:47:34  
 Job time : 58.7593 secs

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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 20.3123 Seconds

(without alignments)  
946.243 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 417  
Sequence: 1 MLSPVLLGLGLAVALPEA.....EDKEDDEEDVPGAKDEL 417

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications: AA:\*

- 1: /cgn2\_6/ptodata/2/pubppa/US08\_NEM\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubppa/PCN\_NEM\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubppa/US06\_NEM\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubppa/US07\_NEM\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubppa/PCrus\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubppa/US09\_NEM\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubppa/US10\_NEM\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubppa/US60\_NEM\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	100.0	417	US-09-906-393A-36	Sequence 36, Appl
2	67	16.1	70	US-09-925-301-1503	Sequence 1503, Ap
3	13	3.1	13	US-09-906-383A-10	Sequence 10, Appl
4	13	3.1	13	US-09-906-393A-11	Sequence 11, Appl
5	13	3.1	13	US-09-906-393A-12	Sequence 12, Appl
6	13	3.1	420	US-09-844-006A-2	Sequence 2, Appl
7	12	2.9	12	US-09-906-393A-6	Sequence 6, Appl
8	11	2.6	11	US-09-906-383A-8	Sequence 8, Appl
9	11	2.6	11	US-09-906-383A-9	Sequence 9, Appl
10	11	2.6	18	US-09-906-383A-9	Sequence 9, Appl
11	11	2.6	18	US-09-554-000-56	Sequence 56, Appl
12	10	2.4	10	US-09-872-832-14	Sequence 14, Appl
13	9	2.2	656	US-09-906-393A-5	Sequence 5, Appl
14	9	2.2	774	US-09-554-000-8	Sequence 8, Appl
15	8	1.9	89	US-09-745-763-115	Sequence 115, App
16	8	1.9	101	US-09-864-761-352A1	Sequence 352A1, A
17	8	1.9	101	US-09-864-761-35359	Sequence 35359, A
18	8	1.9	114	US-09-864-761-36168	Sequence 36168, A
19	8	1.9	122	US-09-844-006A-8	Sequence 8, Appl
			128	US-09-925-300-1757	Sequence 1757, Ap

20	8	1.9	214	US-09-214-881A-1	Sequence 1, Appl
21	8	1.9	214	US-09-214-881A-3	Sequence 3, Appl
22	8	1.9	214	US-09-214-881A-4	Sequence 4, Appl
23	8	1.9	415	US-09-864-761-38147	Sequence 38147, A
24	8	1.9	444	US-09-757-982-14	Sequence 14, Appl
25	8	1.9	506	US-09-814-986-8	Sequence 8, Appl
26	8	1.9	714	US-09-814-986-8	Sequence 8, Appl
27	8	1.9	750	US-09-746-783-86	Sequence 86, Appl
28	8	1.9	1360	US-09-871-916-2	Sequence 2, Appl
29	8	1.9	1404	US-09-862-027-24	Sequence 24, Appl
30	7	1.7	11	US-09-906-393A-7	Sequence 7, Appl
31	7	1.7	17	US-09-906-393A-2	Sequence 2, Appl
32	7	1.7	54	US-09-864-761-39215	Sequence 39215, A
33	7	1.7	54	US-09-864-761-44300	Sequence 44300, A
34	7	1.7	74	US-09-071-838-56	Sequence 56, Appl
35	7	1.7	91	US-09-992-558-349	Sequence 349, App
36	7	1.7	91	US-09-989-735-349	Sequence 349, App
37	7	1.7	91	US-09-989-735-349	Sequence 349, App
38	7	1.7	91	US-09-990-444-349	Sequence 349, App
39	7	1.7	91	US-09-989-730-349	Sequence 349, App
40	7	1.7	91	US-09-990-436-349	Sequence 349, App
41	7	1.7	91	US-09-991-181-349	Sequence 349, App
42	7	1.7	91	US-09-993-687-349	Sequence 349, App
43	7	1.7	91	US-09-989-734-349	Sequence 349, App
44	7	1.7	91	US-09-997-653-349	Sequence 349, App
45	7	1.7	91	US-09-993-667-349	Sequence 349, App

#### ALIGNMENTS

RESULT 1				
QY	US-09-906-393A-36			
	Sequence 36, Application US/09906393A			
	Publication No. US20030039970A1			
	GENERAL INFORMATION:			
	APPLICANT: Wang, Zhou			
	APPLICANT: Xiao, Wuhan			
	TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED			
	FILE REFERENCE: 1720-1-001CIP			
	CURRENT APPLICATION NUMBER: US/09/906,393A			
	CURRENT FILING DATE: 2001-07-16			
	PRIOR APPLICATION NUMBER: 60/218,761			
	PRIOR FILING DATE: 2000-07-17			
	NUMBER OF SEQ ID NOS: 36			
	SOFTWARE: PatentIn version 3.1			
	SEQ ID NO 36			
	LENGTH: 417			
	TYPE: PRT			
	ORGANISM: Homo sapiens			
	US-09-906-393A-36			
Query Match				
Best Local Similarity 100.0%; Score 417; DB 9; Length 417;				
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MLSPVLLGLGLAVALPEAVYFKQFLDGDGWTSMIESKHSKSPGKFLVSSGKFGYDE	60	
DB	1	MLSPVLLGLGLAVALPEAVYFKQFLDGDGWTSMIESKHSKSPGKFLVSSGKFGYDE	60	
QY	61	EDKGLQTSODARFALSAFEPFNKGGTLVVOFTVKEONIDCGGCVTKFPNSLDT	120	
DB	61	EDKGLQTSODARFALSAFEPFNKGGTLVVOFTVKEONIDCGGCVTKFPNSLDT	120	
QY	121	DMHGDSEYNIMGPGICGPTKVVITFNYKKNVLIINKIDCKDDEFTHTLTVRPDN	180	
DB	121	DMHGDSEYNIMGPGICGPTKVVITFNYKKNVLIINKIDCKDDEFTHTLTVRPDN	180	
QY	181	TYEVKINDSVOVSSGSLDDMDLPPKKIKDPDASPEDMDERAKIDDPDPSPEMDKRE	240	
DB	181	TYEVKINDSVOVSSGSLDDMDLPPKKIKDPDASPEDMDERAKIDDPDPSPEMDKRE	240	
QY	241	HIPDDAKKPEMDMDMDGEMEPVIONDEYGEKPKQIDNPDKGTWIHPEIDNPERS	300	

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DB 241 H1PDPKAKPEMDDEMDSEWEPVIONPEYKGMKPROINDNDYKGTWHPIDNPEY 300
      |||||||
QY 301 PPSIAYDNFGVLGIDLMOVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDK 360
      |||||||
DB 301 PPSIAYDNFGVLGIDLMOVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDK 360
      |||||||
QY 361 QDEORLKEEEDKKRKEEEDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
      |||||||
DB 361 QDEORLKEEEDKKRKEEEDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
      |||||||

```

## RESULT 2

```

US-09-925-301-1503
; Sequence 1503, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antipodles
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1503
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1503

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Query Match 16.1%; Score 67; DB 10; Length 70;

Best Local Similarity 100.0%; Pred. No. 1.6e-55; Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 312 GVLGIDLMOVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDKODEORLKEE 371
      |||||||
DB 2 GVLGIDLMOVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDKODEORLKEE 61
      |||||||

```

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QY 372 EDKRRKE 378
      |||||||
DB 62 EDKRRKE 68

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## RESULT 3

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US-09-906-393A-10
; Sequence 10, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-906-393A-10

Query Match 3.1%; Score 13; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 259 GEWEPPVIONPEY 271
      |||||||
DB 1 GEWEPPVIONPEY 13

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## RESULT 4

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US-09-906-393A-11
; Sequence 11, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-11

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Query Match 3.1%; Score 13; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 273 GEWKPROINDNPDY 285
      |||||||
DB 1 GEWKPROINDNPDY 13

```

## RESULT 5

```

US-09-906-393A-12
; Sequence 12, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-12

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Query Match 3.1%; Score 13; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 287 GTWHPIDNPEY 299
      |||||||
DB 1 GTWHPIDNPEY 13

```

## RESULT 6

US-09-844-006A-2



```
; Sequence 2, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051 503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays
US-09-844-006A-2

Query Match          3.1%; Score 13; DB 10; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IPPDPKKPEMD 254
DB 249 IPPDPKKPEMD 261

RESULT 7
US-09-906-393A-6
; Sequence 6, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-906-393A-6

Query Match          2.9%; Score 12; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 157 INKDIRCKDDEF 168
DB 1 INKDIRCKDDEF 12

RESULT 8
US-09-906-393A-8
; Sequence 8, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-906-393A-8

Query Match          2.6%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 PDSKPEMDK 238
DB 1 PDSKPEMDK 11

RESULT 9
US-09-906-393A-9
; Sequence 9, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match          2.6%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 PDKKPEMD 255
DB 1 PDKKPEMD 11

RESULT 10
US-09-554-000-56
; Sequence 56, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-554-000-56

Query Match          2.6%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 VPLLGLGLG 15  
Db 5 VPLLGLGLG 15

RESULT 11  
US-09-872-832-14  
; Sequence 14, Application US/09872832  
; Patent No. US20020131960A1  
; GENERAL INFORMATION:  
; APPLICANT: Memorial Sloan-Kettering Cancer Center  
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF  
; FILE REFERENCE: 830002-2003.1  
; CURRENT APPLICATION NUMBER: US/09/872,832  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: 60/209,157  
; PRIOR FILING DATE: 2000-02-06  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 14  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-872-832-14

Query Match 2.4%; Score 10; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTSPVLLG 10  
Db 1 MLTSPVLLG 10

RESULT 12  
US-09-906-393A-5  
; Sequence 5, Application US/09906393A  
; Publication No. US20030039970A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906,393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-906-393A-5

Query Match 2.4%; Score 10; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0071;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 CGGGYVKLP 114  
Db 1 CGGGYVKLP 10

RESULT 13  
US-09-554-000-8  
; Sequence 8, Application US/09554000  
; Patent No. US20020165364A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; TITLE OF INVENTION: DETECTION OF ANALYTES

FILE REFERENCE: 07257/042001  
; CURRENT APPLICATION NUMBER: US/09/554,000  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 08/818,252  
; PRIOR FILING DATE: 1997-03-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 8  
; LENGTH: 656  
; TYPE: PRT  
; ORGANISM: Aequorea victoria  
US-09-554-000-8

Query Match 2.2%; Score 9; DB 9; Length 656;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLLGLGLG 13  
Db 5 VPLLGLGLG 13

RESULT 14  
US-09-745-763-115  
; Sequence 115, Application US/09745763  
; Patent No. US20020065394A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; McCoy, John M.  
; LaVallie, Edward R.  
; Collins-Racie, Lisa A.  
; Evans, Cheryl  
; Merberg, David  
; Treacy, Maurice  
; Spaulding, Vikki  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 219  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/745,763  
; FILING DATE: 18-Jun-2000  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sprunger, Suzanne A.  
; REGISTRATION NUMBER: 41,323  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8284  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 774 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:  
US-09-745-763-115

Query Match 2.2%; Score 9; DB 10; Length 774;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 392 DEDEDEED 400  
 |||||  
 Db 615 DEDEDEED 623

RESULT 15  
 US-09-864-761-35241  
 ; Sequence 35241, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 FILE REFERENCE: Aeonica-X-1  
 CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 09/608,408  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203  
 PRIOR FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 49117  
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
 SEQ ID NO 35241  
 LENGTH: 89  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: MAP TO AL034548.24  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4  
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7  
 US-09-864-761-35241

Query Match 1.9%; Score 8; DB 10; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 3.7;  
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;

OY 374 KKKKEEE 381  
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 Db 65 KKKKEEE 72

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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 15.9312 Seconds  
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Title: US-09-807-148-2  
Perfect score: 417  
Sequence: 1 MLTSPVLLGLGLVAEPA.....EEDKEDEEDVPGAKDEL 417

Scoring table: OLIGO  
Gapop 60.0 , Gapept 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	100.0	417	1	CRTC_HUMAN
2	182	43.6	418	1	P27797 homo sapien
3	93	22.3	416	1	P15253 oryctolagus
4	93	22.3	416	1	CRTC_MOUSE
5	62	14.9	400	1	CRTL_BOVIN
6	62	14.9	421	1	CRT2_BOVIN
7	25	6.0	105	1	CRTC_PIG
8	23	4.6	388	1	RAL1_ONCVO
9	19	4.6	406	1	CRTC_DROME
10	17	4.1	395	1	CRTC_CAEEL
11	14	3.4	393	1	CRTC_SCMA
12	13	3.1	401	1	CRTC_EUGGR
13	13	3.1	415	1	CRTC_RICCO
14	13	3.1	420	1	CRTC_MAIZE
15	11	2.6	416	1	CRTC_NICPL
16	11	2.6	421	1	CRTC_PBUAR
17	11	2.6	528	1	CAX2_ARATH
18	11	2.6	530	1	CAX1_ARATH
19	11	2.6	540	1	CALX_HELTV
20	11	2.6	546	1	CALX_SOYBN
21	11	2.6	551	1	CALX_PEA
22	10	2.4	420	1	CRTC_CHIRE
23	10	2.4	424	1	CRTC_CORYSA
24	9	2.2	13	1	CRTC_BOVIN
25	9	2.2	149	1	CRTC_CANFA
26	9	2.2	149	1	HMGL_VICPA
27	9	2.2	361	1	APEA_DICDI
28	9	2.2	412	1	FKR4_SPOR
29	9	2.2	416	1	CRTC_BERST
30	9	2.2	416	1	CRTC_BETVU
31	9	2.2	424	1	CRT2_ARATH
32	9	2.2	424	1	CRTC_DICDI
33	9	2.2	425	1	CRTL_ARATH

34	9	2.2	700	1	CH60_PLAFC	P34940 plasmodium
35	9	2.2	712	1	NUCL_RAT	P13383 rattus norv
36	8	1.9	134	1	CLX2_NARJA	O42105 narke japon
37	8	1.9	191	1	RPOE-STREP	P58053 streptococ
38	8	1.9	211	1	HMIX_HUMAN	Q9UGV6 homo sapien
39	8	1.9	214	1	HMGL_BOVIN	P10103 bos taurus
40	8	1.9	214	1	HMGL_HUMAN	P09429 homo sapien
41	8	1.9	214	1	HMGL_PIG	P12682 sus scrofa
42	8	1.9	329	1	COR4_HUMAN	Q9BXJ3 homo sapien
43	8	1.9	357	1	YML9_YEAST	Q03208 saccharomyc
44	8	1.9	364	1	IE68_PPRKA	P24827 pseudorabie
45	8	1.9	377	1	PEXE_HUMAN	O75381 homo sapien

# ALIGNMENTS

RESULT 1						
CRTC_HUMAN	STANDARD:	PRT:	417	AA.		
ID						
AC	P27797:					
DT	01-AUG-1992 (Rel. 23, Created)					
DT	01-AUG-1992 (Rel. 23, Last sequence update)					
DT	15-JUN-2002 (Rel. 41, Last annotation update)					
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60).					
GN	CALR OR CRTC.					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=92013129; PubMed=1919005;					
RA	Rokach L.A., Haselby J.A., Mellof J.F., Smeenk R.J., Unnasch T.R.,					
RA	Greene B.M., Hoch S.O.;					
RT	"Characterization of the autoantigen calreticulin.";					
RL	J. Immunol. 147:3031-3039(1991).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=90237213; PubMed=2332496;					
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,					
RA	Bachinski L.L., Itoh Y., Stelliato M.J., Sontheimer R.D.,					
RT	Capra J.D.;					
RT	"Molecular cloning, expression, and chromosome 19 localization of a					
RT	human Ro/SS-A autoantigen.";					
RL	J. Clin. Invest. 85:1379-1391(1990).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=92129342; PubMed=1733953;					
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;					
RT	"The 5'-flanking region of the human calreticulin gene shares					
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase					
RT	promoters.";					
RL	J. Biol. Chem. 267:2557-2562(1992).					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RA	Liu J., Peng X., Yuan J., Qiang B.;					
RT	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.					
RN	[5]					
RP	SEQUENCE FROM N.A.					
RA	Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;					
RT	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.					
RN	[6]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Eye, Pancreas, and Skin;					
RA	Strusberg R.;					
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.					
RN	[7]					
RP	SEQUENCE OF 18-36.					
RA	MEDLINE=92002034; PubMed=1911778;					
RA	Rojiani M.V., Filalay B.B., Gray V., Dedhar S.;					
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A					
RT	antigen (calreticulin) with a highly conserved amino acid sequence in					

RT the cytoplasmic domain of integrin alpha subunits.";  
 RN Biochemistry 30:9859-9866(1991).  
 RN [8]  
 RX SEQUENCE OF 18-32.  
 RX MEDLINE-90380058; PubMed-2400400;  
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;  
 RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein  
 RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60  
 RT cells.";  
 RL Biochem. J. 270:545-548(1990).  
 RN [9]  
 RP SEQUENCE OF 18-28.  
 RP TISSUE-LIVER;  
 RX MEDLINE-93162045; PubMed-1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 RA Pasquali C., Sanchez G.J., Tissot J.-D., Bjellqvist B., Vargas R.,  
 RA Appel R.D., Hughes G.J.;  
 RT "Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.";  
 RL Electrophoresis 13:992-1001(1992).  
 RN [10]  
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
 RP TISSUE-Keratinocytes;  
 RX MEDLINE-93162043; PubMed-1286667;  
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
 RA Vandekerckhove J.;  
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
 RT protein database of normal human epidermal keratinocytes.";  
 RL Electrophoresis 13:960-969(1992).  
 RN [11]  
 RP SEQUENCE OF 18-26.  
 RP TISSUE-Colon carcinoma;  
 RX MEDLINE-97295306; PubMed-9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
 RT "A two-dimensional gel database of human colon carcinoma proteins.";  
 RL Electrophoresis 18:605-613(1997).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro  
 CC autoantigen.  
 CC -----  
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 CC -----  
 DR EMBL: M84739; AAA51916.1; -;  
 DR EMBL: M32294; AAA36582.1; -;  
 DR EMBL: AY047586; AAL13126.1; -;  
 DR EMBL: AD000092; AAB51176.1; -;  
 DR EMBL: BC002500; AAH02500.1; -;  
 DR EMBL: BC007911; AAH07911.1; -;  
 DR EMBL: BC020493; AAH20493.1; -;  
 DR PIR: A37047; A37047.  
 DR PIR: S11475; S11475.  
 DR PIR: A42330; A42330.  
 DR PIR: A46452; A46452.  
 DR SWISS-2DPAGE: P27797; HUMAN.  
 DR Aatrus/Ghent-2DPAGE: 9401; IEF.  
 DR PHMA-2DPAGE: P27797; -;  
 DR PHCI-2DPAGE: P27797; -;  
 DR HSC-2DPAGE: P27797; HUMAN.  
 DR Stena-2DPAGE: P27797; -;  
 DR Genew; HGNC:1455; CALR.  
 DR MIM: 109091; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.

DR Pfam: PF00262; Calreticulin; 1.  
 DR PRINTS; PRO00626; CALRETICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum, Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1  
 FT CHAIN 17  
 FT DOMAIN 18 417 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;  
 Query Match 100.0%; Score 417; DB 1; Length 417;  
 Best local similarity 100.0%; Pred. No. 0;  
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLTSVLLGLGLGLAVALPAVYKKEQFLDGDGWTSMISKHKSDFGKFLVSSGKRYGDE 60  
 DB 1 MLTSVLLGLGLGLAVALPAVYKKEQFLDGDGWTSMISKHKSDFGKFLVSSGKRYGDE 60  
 QY 61 EKDKGLQTSQDAARFALSAFEPFSKNGQTLVQVTFYKHEQNIIDCGGKYKFLPNSLDOT 120  
 DB 61 EKDKGLQTSQDAARFALSAFEPFSKNGQTLVQVTFYKHEQNIIDCGGKYKFLPNSLDOT 120  
 QY 121 DMHGSEVYIMFGPDICGCGTKKVHYTFYKGNVLIINDIRCKODEFTHLTYLYRPDN 180  
 DB 121 DMHGSEVYIMFGPDICGCGTKKVHYTFYKGNVLIINDIRCKODEFTHLTYLYRPDN 180  
 QY 121 DMHGSEVYIMFGPDICGCGTKKVHYTFYKGNVLIINDIRCKODEFTHLTYLYRPDN 180  
 DB 121 DMHGSEVYIMFGPDICGCGTKKVHYTFYKGNVLIINDIRCKODEFTHLTYLYRPDN 180  
 QY 181 YTEVKIDNSQVESGSLDDMDFLPPKKIKDPPASKEPMDERAKIDPTDSKPEDMDKPE 240  
 DB 181 YTEVKIDNSQVESGSLDDMDFLPPKKIKDPPASKEPMDERAKIDPTDSKPEDMDKPE 240  
 QY 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKRPQIDNPDYKGTWHPIDNPEYS 300  
 DB 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKRPQIDNPDYKGTWHPIDNPEYS 300  
 QY 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKRPQIDNPDYKGTWHPIDNPEYS 300  
 DB 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKRPQIDNPDYKGTWHPIDNPEYS 300  
 QY 301 PPSITAYNFGVLGLDLMQVKSQTFFDNFLTNDVAAYEERFENFTWGTAKAEKOMKDK 360  
 DB 301 PPSITAYNFGVLGLDLMQVKSQTFFDNFLTNDVAAYEERFENFTWGTAKAEKOMKDK 360  
 QY 361 QDEEQLKEEEDKKRKEEAEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417  
 DB 361 QDEEQLKEEEDKKRKEEAEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417  
 RESULT 2  
 CRTC\_RABIT  
 ID CRTC\_RABIT STANDARD; PRT; 418 AA.  
 AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Calreticulin precursor (CRP5) (Calregulin) (HACBP) (Erp60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=slow-twitch skeletal muscle;  
 RX MEDLINE=90094320; PubMed=2600080;  
 RA Fliegel L., Burns K., MacLennan D.H., Reilmeyer R.A.F., Michalak M.;  
 RT "Molecular cloning of the high affinity calcium-binding protein  
 (calreticulin) of skeletal muscle sarcoplasmic reticulum.";  
 RL J. Biol. Chem. 264:21522-21528(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=fast-twitch skeletal muscle;  
 RX MEDLINE=91282795; PubMed=2059224;  
 RA Fliegel L., Michalak M.;  
 RT "Fast-twitch and slow-twitch skeletal muscles express the same  
 isoform of calreticulin.";  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 RN [3]  
 RP SEQUENCE OF 18-36.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [4]  
 RP SEQUENCE OF 18-46.  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Bakes S., Shemanko C., Carpenter M.R., Smillie L.,  
 Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 reticulum.";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=92002038; PubMed=1911780;  
 RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 monooxygenase and calreticulin.";  
 RL Biochemistry 30:9892-9900(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: J05138, AAA31188.1; .  
 DR PIR: A34154; A34154.  
 DR PIR: C33208; C33208.  
 DR PIR: D33208; D33208.  
 DR PIR: E33208; E33208.  
 DR PIR: F33208; F33208.  
 DR PIR: S13046; S13046.  
 DR PIR: S13047; S13047.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00014; ER\_TARGET.1.  
 DR PROSITE: PS00803; CALRETICULIN.1; 1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT.3.  
 RP

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 418 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 418 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 202 220 1-2.  
 FT REPEAT 220 227 1-3.  
 FT REPEAT 227 238 1-4.  
 FT REPEAT 238 255 2-1.  
 FT REPEAT 255 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 297 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 415 418 PREVENT SECRETION FROM ER.  
 FT VARIANT 35 35 E -> D.  
 FT CONFLICT 90 90 P -> T (IN REF. 5).  
 SQ SEQUENCE 418 AA; 48275 MM; B6082689DC763A6 CRC64;  
 Query Match 43.6%; Score 182; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-158;  
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 121 DMHGDSEYIMFGPDICGCTKVVHVFYKGNVLINKDIRCKDDEPHLYTLVLRPN 180  
 DB 121 DMHGDSEYIMFGPDICGCTKVVHVFYKGNVLINKDIRCKDDEPHLYTLVLRPN 180  
 QY 181 TYEVKIDNSQVSGSLIEDMDFLPKIKDPASKEPMDERAKIDDPDSKPEMDKPE 240  
 DB 181 TYEVKIDNSQVSGSLIEDMDFLPKIKDPASKEPMDERAKIDDPDSKPEMDKPE 240  
 QY 241 HIPDPKAKPEMDDEMDPEPPYIONPEYKGEKPROIDNPDKYKGIWIHPEIDNPEYS 300  
 DB 241 HIPDPKAKPEMDDEMDPEPPYIONPEYKGEKPROIDNPDKYKGIWIHPEIDNPEYS 300  
 QY 301 PD 302  
 DB 301 PD 302  
 DB 301 PD 302  
 RESULT 3  
 CRIC\_MOUSE STANDARD; PRT; 416 AA.  
 ID P14211;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).  
 GN CALR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.  
 RC STRAIN-BALB/c; TISSUE=Liver;  
 RX MEDLINE=90059955; PubMed=2563110;  
 RA Smith M.J., Koch G.L.E.;  
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,  
 HACBP), a major calcium binding ER/SR protein.";  
 RL EMBO J. 8:3581-3586(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93013037; PubMed=1398135;  
 RA Mazzarelli R.A., Gold P., Cunningham M., Green M.;  
 RT "Determination of the sequence of an expressible cDNA clone encoding  
 ERp60/calregulin by the use of a novel nested set method.";  
 RL Gene 120:217-225(1992).  
 RN [3]  
 RP SEQUENCE OF 18-38.

RC TISSUE-Fibroblast;  
 RA MEDLINE=95009907; PubMed=7523108;  
 RT Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL: X14926; CA33053.1; -;  
 DR EMBL: M92988; AAA37569.1; -;  
 DR PIR: S06763; S06763.  
 DR PIR: JC1444; JC1444.  
 DR SWISS-2DPAGE: P14211; MOUSE.  
 DR MGD: MGI:88252; CALR.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin\_1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 416 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.  
 FT DISLFD 137 163 BY SIMILARITY.  
 FT SITE 413 416 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D CRC64;  
 Query Match 22.3%; Score 93; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-77;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 121 DMHGSSEYINFGPDICGGTGGKRVHIFNVYKGNVLINRDKRDEFFHLTLIYRPDN 180  
 Db 121 DMHGSSEYINFGPDICGGTGGKRVHIFNVYKGNVLINRDKRDEFFHLTLIYRPDN 180  
 Oy 181 TYEVKIDNSQVESGSLDDMDLPPKKIKDPDA 213  
 Db 181 TYEVKIDNSQVESGSLDDMDLPPKKIKDPDA 213  
 RESULT 4  
 CRTC\_RAT STANDARD; PRT; 416 AA.  
 AC CRTC\_RAT P10452;  
 DT 01-MAR-1989 (rel. 10, Created)

DT 01-NOV-1990 (rel. 16, last sequence update)  
 DT 01-NOV-1997 (rel. 35, last annotation update)  
 DE Calreticulin precursor (CRP5) (Calregulin) (HACBP) (ERP60) (CALBP)  
 DE (Calcium-binding protein 3) (CABP3).  
 GN CALR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE=brain cortex;  
 RX MEDLINE=90370496; PubMed=2395661;  
 RA Murthy K.K., Banville D., Strikant C.B., Carrier F., Bell A.,  
 RA Holmes C., Patel Y.C.;  
 RT "Structural homology between the rat calreticulin gene product and  
 RT the Onchocerca volvulus antigen Ral-1.";  
 RL Nucleic Acids Res. 18:4933-4933(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE=liver;  
 RX MEDLINE=95181573; PubMed=7876339;  
 RA Soenichsen B., Fuellkrug J., Van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Mieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain  
 RT calreticulin in the endoplasmic reticulum.";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 RN [4]  
 RP SEQUENCE OF 270-358 FROM N.A.  
 RC STRAIN-Sprague-Dawley;  
 RA Lone Y.C., Bailly A., Latruffe N.;  
 RL Submitted (DEC-1988) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 18-29.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [6]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN-Sprague-Dawley; TISSUE=Testis;  
 RX MEDLINE=92360010; PubMed=1497655;  
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
 RT "Calreticulin is present in the acrosome of spermatozoa of rat  
 RT testis.";  
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
 RN [7]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN-LEC; TISSUE=Liver;  
 RX MEDLINE=94072621; PubMed=8251535;  
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
 RA Kamataki T.;  
 RT "Identification of protein disulfide isomerase and calreticulin as  
 RT autoimmune antigens in LEC strain of rats.";  
 RL Biochim. Biophys. Acta 1158:339-344(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- CAUTION: WAS ORIGINALLY (REF 2) THOUGHT TO BE D-BETA-  
 CC HYDROXYBUTYRATE DEHYDROGENASE.



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-----  
DR EMBL; D78308; BAA11345.1; -;  
DR EMBL; X53363; CAA37446.1; -;  
DR EMBL; X13702; CAA31987.1; ALT\_SEQ.  
DR EMBL; X79327; CAA55890.1; -;  
DR PIR; S04867; S04867.  
DR PIR; S11205; S11205.  
DR PIR; S13045; S13045.  
DR PIR; A49176; A49176.  
DR PIR; S45036; S45036.  
DR PIR; JH0819; JH0819.  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam; PF00262; Calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
KW SIGNAL  
FT CHAIN 1 17  
FT DOMAIN 18 416 CALRETICULIN.  
FT DOMAIN 18 197 N-DOMAIN.  
FT DOMAIN 198 308 P-DOMAIN.  
FT DOMAIN 309 416 C-DOMAIN.  
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
FT REPEAT 191 202 1-1.  
FT REPEAT 210 221 1-2.  
FT REPEAT 227 238 1-3.  
FT REPEAT 244 255 1-4.  
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
FT REPEAT 259 269 2-1.  
FT REPEAT 273 283 2-2.  
FT REPEAT 287 297 2-3.  
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.  
FT DISULFID 137 163 BY SIMILARITY.  
FT SITE 413 416 PREVENT SECRETION FROM ER.  
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;  
  
Query Match 22.3%; Score 93; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 2.4e-77;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 121 DMHGDSSEYINMGPDICGPGTKRVHVFNYGKNVLLINKDIRCKDDEFTHTLTVRPD 180  
DB 121 DMHGDSSEYINMGPDICGPGTKRVHVFNYGKNVLLINKDIRCKDDEFTHTLTVRPD 180  
QY 181 TTEVKINDSQVESGSLSDNDPLPKKIKDPDA 213  
DB 181 TTEVKINDSQVESGSLSDNDPLPKKIKDPDA 213  
  
RESULT 5  
CRT1\_BOVIN  
ID CRT1\_BOVIN STANDARD; PRT; 400 AA.  
AC P52193;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).  
OS Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94183174; PubMed=8135753;  
RA Matsuka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;  
RT "Covalent structure of bovine brain calreticulin";  
RL Biochem. J. 298:435-442(1994).  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam; PF00262; Calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR Endoplasmic reticulum; Calcium-binding; Repeat; glycoprotein.  
KW DOMAIN 1 180  
FT DOMAIN 181 291 N-DOMAIN.  
FT DOMAIN 292 400 P-DOMAIN.  
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.  
FT REPEAT 174 185 1-1.  
FT REPEAT 193 204 1-2.  
FT REPEAT 210 221 1-3.  
FT REPEAT 227 238 1-4.  
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.  
FT REPEAT 242 252 2-1.  
FT REPEAT 256 266 2-2.  
FT REPEAT 270 280 2-3.  
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.  
FT DISULFID 120 146  
FT CARBOHYD 162 162  
FT SITE 397 400 N-LINKED (GLCNAC. . .).  
SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;  
  
Query Match 14.9%; Score 62; DB 1; Length 400;  
Best Local Similarity 100.0%; Pred. No. 5.1e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 117 LDQTDHMGDSSEYINMGPDICGPGTKRVHVFNYGKNVLLINKDIRCKDDEFTHTLTV 176  
DB 100 LDQTDHMGDSSEYINMGPDICGPGTKRVHVFNYGKNVLLINKDIRCKDDEFTHTLTV 159  
QY 177 RP 178  
DB 160 RP 161  
  
RESULT 6  
CRT2\_BOVIN  
ID CRT2\_BOVIN STANDARD; PRT; 421 AA.  
AC P42918;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).  
OS Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93385184; PubMed=8373827;  
RA Liu N., Fine R.E., Johnson R.J.;  
RT "Comparison of cDNAs from bovine brain coding for two isoforms of

FT Calreticulin.  
 CC Biochim. Biophys. Acta 1202:70-76(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC EMBL: L13462; AAC37307.1; -  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN.1; 1.  
 DR PROSITE: PS00804; CALRETICULIN.2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 34  
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.  
 FT DOMAIN 35 201 N-DOMAIN.  
 FT DOMAIN 202 312 P-DOMAIN.  
 FT DOMAIN 313 421 C-DOMAIN.  
 FT REPEAT 195 259 4 X APPROXIMATE REPEATS.  
 FT REPEAT 206 259 1-1.  
 FT REPEAT 214 225 1-2.  
 FT REPEAT 231 242 1-3.  
 FT REPEAT 248 259 1-4.  
 FT REPEAT 263 301 3 X APPROXIMATE REPEATS.  
 FT REPEAT 263 273 2-1.  
 FT REPEAT 277 287 2-2.  
 FT REPEAT 291 301 2-3.  
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.  
 FT DISULFID 141 167 BY SIMILARITY.  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 418 421 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;  
 Query Match 14.9%; Score 62; DB 1; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-49;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 117 LDQTMHGDSEYNIMFGPGTGRKKNVIFNYKGNVLRKDKDEFTHTLTIV 176  
 DB 121 LDQTMHGDSEYNIMFGPGTGRKKNVIFNYKGNVLRKDKDEFTHTLTIV 180  
 QY 177 RP 178  
 DB 181 RP 182  
 RESULT 7  
 CRTC\_PIG STANDARD; PRT; 105 AA.  
 AC P28491;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP50)  
 DE (Fragment).  
 GN CALR.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_Taxid=9823;  
 RN (1)  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=Small intestine;  
 RX MEDLINE=96327607; PubMed=8672129;  
 RA Winteroe A.K., Fredholm M., Davies W.;  
 RT "Evaluation and characterization of a porcine small intestine cDNA  
 RT library: analysis of 839 clones."  
 RL Mamm. Genome 7:509-517(1996).  
 RN (2)  
 RP SEQUENCE OF 18-32.  
 RC TISSUE=uterus;  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Baxsh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum."  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 CC EMBL: F14591; CAA23142.1; -  
 DR PIR: B33208; B33208.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin.1.  
 DR ProDom: PD001866; Calreticulin.1.  
 DR PROSITE: PS00803; CALRETICULIN.1; PARTIAL.  
 DR PROSITE: PS00804; CALRETICULIN.2; PARTIAL.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 >105 CALRETICULIN.  
 FT DOMAIN 18 >105 N-DOMAIN.  
 FT NON\_TER 105 105  
 SQ SEQUENCE 105 AA; 11958 MW; D203B53FE36BDE1E CRC64;  
 Query Match 6.0%; Score 25; DB 1; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
 Matches 25; Conservative 100; Mismatches 0; Indels 0; Gaps 0;  
 QY 81 FEPFSNKGOTLVVQFTVKHEQNIDC 105  
 DB 81 FEPFSNKGOTLVVQFTVKHEQNIDC 105  
 RESULT 8  
 RAL1\_ONCVO STANDARD; PRT; 388 AA.  
 AC P11012;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE RAL-1 protein precursor (41 kDa larval antigen).  
 GN RAL1.  
 OS Onchocerca volvulus.  
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 CC Onchocercidae; Onchocerca.  
 CC NCBI\_Taxid=6282;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94341871; PubMed=7520419;

RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;  
 RT "Epitopes of the Onchocerca volvulus RALI antigen, a member of the  
 RT calreticulin family of proteins, recognized by sera from patients  
 RT with onchocerciasis";  
 RL Infect. Immun. 62:3696-3704(1994).  
 RN (2)  
 RP SEQUENCE OF 53-388 FROM N.A.  
 RX MEDLINE=88273584; PubMed=2455736;  
 RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;  
 RT "Isolation and characterization of expression cDNA clones encoding  
 RT antigens of Onchocerca volvulus infective larvae";  
 RL J. Clin. Invest. 82:262-269(1988).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL; M20565; AAA59056.1; -;  
 DR PIR; A32507; A32507.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Calcium-binding; Repeat; Antigen; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 388 RAL-1 PROTEIN.  
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
 FT REPEAT 189 200 1-1.  
 FT REPEAT 208 219 1-2.  
 FT REPEAT 225 236 1-3.  
 FT REPEAT 242 253 1-4.  
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
 FT REPEAT 257 267 2-1.  
 FT REPEAT 271 281 2-2.  
 FT REPEAT 285 295 2-3.  
 FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
 FT DISURFD 135 161 BY SIMILARITY.  
 SQ SEQUENCE 388 AA; 45298 MW; 9537E298A2D31C06 CRC64;  
 Query Match 5.5%; Score 23; DB 1; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 2,2e-13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 232 KPEWDKPEHIPPDPKKRPDMD 254  
 Db 230 KPEWDKPEHIPPDPKKRPDMD 252  
 RESULT 9  
 CRTC\_DROME STANDARD; PRT; 406 AA.  
 AC P29413; G9VHA3;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor (CRF55) (Calregulin) (HACBP).  
 OS CRC OR CG9429.  
 GN Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 RX NCBI [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=93208374; PubMed=1296819;

RA Smith M.J.;  
 RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a  
 RT calreticulin homologue";  
 RL DNA Seq. 3:247-250(1992).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP SEQUENCE OF 91-124 AND 182-220.  
 RP MEDLINE=90307981; PubMed=2365822;  
 RX McCauliffe D.P., Zappi E., Lieu T.S., Michalak M., Sonthheimer R.D.,  
 RA Capra J.D.;  
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
 RT highly homologous with onchocercal RAL-1 antigen and an aplasia  
 RT 'memory molecule'";  
 RL J. Clin. Invest. 86:332-335(1990).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X64461; CA45791.1; -;  
 DR EMBL; AE003683; AA54416.1; -;  
 DR PIR; A37158; A37158.  
 DR FlyBase; FBgn0005585; CRC.  
 DR InterPro; IPR001580; Calreticulin.



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 CC -----  
 DR EMBL: M93097; AAA29854.1; -;  
 DR EMBL: L24159; AAA19024.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; Calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal; Glycoprotein.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 393 CALRETICULIN.  
 FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.  
 FT REPEAT 189 200 1-1.  
 FT REPEAT 209 220 1-2.  
 FT REPEAT 225 236 1-3.  
 FT REPEAT 243 254 1-4.  
 FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.  
 FT REPEAT 257 267 2-1.  
 FT REPEAT 271 281 2-2.  
 FT REPEAT 285 295 2-3.  
 FT CARBOHYD 27 27 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT DISULFID 135 161 BY SIMILARITY.  
 FT SITE 390 393 PREVENT SECRETION FROM ER.  
 FT CONFLICT 89 90 MV -> IL (IN REF. 2).  
 FT CONFLICT 188 207 MISSING (IN REF. 2).  
 FT CONFLICT 378 378 Y -> D (IN REF. 2).  
 SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;  
 Query Match 3.4%; Score 14; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 141 TKVHVHFNKGN 154  
 DB 139 TKVHVHFNKGN 152  
 RESULT 12  
 CRTC\_EUGGR STANDARD: PRT; 401 AA.  
 AC 09ZNY3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 DE Euglena gracilis.  
 OS Eukaryota; Euklenozoa; Euglenida; Euglenales; Euglena.  
 OC NCBI\_TaxID=3039;  
 RN NCBI\_TaxID=3039;  
 RP SEQUENCE FROM N.A.  
 RA Navazzio L., Baldan B., Martin W., Mariani P.;  
 RT "Evidence for conservation of a calcium homeostatic component:  
 RT purification characterization and cloning of calreticulin from Euglena  
 RT gracilis.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Y09816; CA70945.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; FALSE NEG.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 401 CALRETICULIN.  
 FT SITE 398 401 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 401 AA; 45910 MW; 056B074C16292674 CRC64;  
 Query Match 3.1%; Score 13; DB 1; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.00031;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 317 DLMQVKSCTIFDN 329  
 DB 314 DLMQVKSCTIFDN 326  
 RESULT 13  
 CRTC\_RICCO STANDARD: PRT; 415 AA.  
 AC P93508;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 DE Ricinus communis (Castor bean).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Euphorbiales; Ricinus.  
 OC NCBI\_TaxID=3988;  
 RN NCBI\_TaxID=3988;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97435975; PubMed=9290642;  
 RA Coughlan S.J., Hastings C., Winfrey R. Jr.;  
 RT "Cloning and characterization of the calreticulin gene from Ricinus  
 RT communis L.";  
 RL Plant Mol. Biol. 34:897-911(1997).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U74631; AAB71420.1; -;  
 DR EMBL: U74630; AAB71419.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal; Glycoprotein.

FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 415 CALRETICULIN.  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 415 AA: 47522 MW: D55F452E76C7F8C CRC64;

Query Match 3.1%; Score 13; DB 1; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IPDPAPKPEMD 254  
 DB 244 IPDPAPKPEMD 256

## RESULT 14

CRTC\_MAIZE STANDARD; PRT; 420 AA.

AC 095P22;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 GN CRT.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
 OC Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wyatt W.E., Tsou P.-L., Robertson D.;  
 RT "Effects of altered expression of the calcium-binding protein  
 RT calreticulin in Arabidopsis thaliana."  
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC -1- LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----

DR EMBL: AF190454; AAF01470.1;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; FALSE\_NEG.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 420 CALRETICULIN.  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 420 AA: 47939 MW: E73B7F43E7494735 CRC64;

Query Match 3.1%; Score 13; DB 1; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IPDPAPKPEMD 254  
 DB 249 IPDPAPKPEMD 261

## RESULT 15

CRTC\_NICPL STANDARD; PRT; 416 AA.

AC 040401;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 GN CAL.  
 OS Nicotiana glauca (Leadwort-leaved tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4092;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borisjuk N., Borisjuk L., Adler K., Sitallo L., Tewes A.,  
 RA Mantelupfel R.;  
 RT "Differential expression of calreticulin during somatic and  
 RT zygotic embryogenesis of Nicotiana glauca.";  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC -1- LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----

DR EMBL: Z71395; CA95999.1;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 2.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 416 CALRETICULIN.  
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 416 AA: 47481 MW: 5026F3152B8828C0 CRC64;

Query Match 2.6%; Score 11; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 DPDPAPKPEMD 254  
 DB 253 DPDPAPKPEMD 263

Search completed: March 14, 2003, 20:45:03  
 Job time : 17.9312 secs

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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 23.4986 Seconds  
(without alignments) 522.132 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 417  
Sequence: 1 MLTSLVPLLGLGLVAEPA.....EEDKEDEEDVPGQANDEL 417

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: Issued Patents-AA:\*  
2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	4.6	19	1	US-08-335-198-10	Sequence 10, Appl
2	17	4.1	17	1	US-08-045-261-9	Sequence 9, Appl
3	15	3.6	18	2	US-08-818-253-61	Sequence 61, Appl
4	14	3.4	15	3	US-08-946-026-53	Sequence 53, Appl
5	13	3.1	415	4	US-08-675-816-2	Sequence 2, Appl
6	12	2.9	12	1	US-08-045-261-2	Sequence 2, Appl
7	11	2.6	12	1	US-08-045-261-1	Sequence 1, Appl
8	11	2.6	12	1	US-08-045-261-4	Sequence 4, Appl
9	11	2.6	18	2	US-08-818-253-56	Sequence 56, Appl
10	11	2.6	18	4	US-08-818-252-56	Sequence 56, Appl
11	11	2.6	542	4	US-08-675-816-6	Sequence 6, Appl
12	10	2.4	12	1	US-08-045-261-3	Sequence 3, Appl
13	10	2.4	12	1	US-08-045-261-5	Sequence 5, Appl
14	10	2.4	12	1	US-08-045-261-6	Sequence 6, Appl
15	10	2.4	17	1	US-08-335-198-9	Sequence 9, Appl
16	9	2.2	412	2	US-08-741-134-2	Sequence 2, Appl
17	9	2.2	656	2	US-08-818-253-8	Sequence 8, Appl
18	9	2.2	656	4	US-08-818-252-8	Sequence 8, Appl
19	8	1.9	193	4	US-09-149-476-406	Sequence 406, App
20	8	1.9	369	2	US-08-723-415B-4	Sequence 4, Appl
21	8	1.9	369	4	US-09-189-627A-4	Sequence 4, Appl
22	8	1.9	369	4	US-09-710-861-4	Sequence 4, Appl
23	8	1.9	370	2	US-08-723-415B-6	Sequence 6, Appl
24	8	1.9	370	4	US-09-189-627A-6	Sequence 6, Appl
25	8	1.9	370	4	US-09-710-861-6	Sequence 6, Appl
26	8	1.9	385	2	US-08-723-415B-8	Sequence 8, Appl
27	8	1.9	385	4	US-09-189-627A-8	Sequence 8, Appl

28	8	1.9	385	4	US-09-710-861-8	Sequence 8, Appl
29	8	1.9	444	3	US-09-221-235-14	Sequence 14, Appl
30	8	1.9	444	3	US-09-221-928-14	Sequence 14, Appl
31	8	1.9	444	4	US-09-221-527-14	Sequence 14, Appl
32	8	1.9	444	4	US-09-221-236-14	Sequence 14, Appl
33	8	1.9	444	4	US-09-221-416-14	Sequence 14, Appl
34	8	1.9	444	4	US-09-221-245-14	Sequence 14, Appl
35	8	1.9	444	4	US-09-163-115-14	Sequence 14, Appl
36	8	1.9	444	4	US-09-221-528-14	Sequence 14, Appl
37	8	1.9	444	4	US-09-593-553-14	Sequence 14, Appl
38	8	1.9	444	4	US-09-221-237-14	Sequence 14, Appl
39	8	1.9	446	2	US-08-723-415B-2	Sequence 2, Appl
40	8	1.9	446	4	US-09-189-627A-2	Sequence 2, Appl
41	8	1.9	446	4	US-09-710-861-2	Sequence 2, Appl
42	8	1.9	460	1	US-08-630-592-7	Sequence 7, Appl
43	8	1.9	460	1	US-08-714-991-7	Sequence 7, Appl
44	8	1.9	460	3	US-09-032-365A-8	Sequence 8, Appl
45	8	1.9	506	1	US-08-631-200-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-08-335-198-10  
Sequence 10, Application US/08335198  
Patent No. 5657454  
GENERAL INFORMATION:  
APPLICANT: Harley, John B.  
TITLE OF INVENTION: Assays and Treatments for Autoimmune  
TITLE OF INVENTION: Diseases  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Ste. 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309-4539  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,198  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/648205  
FILING DATE: 01-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF 11ACIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
AMT-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-335-198-10  
Query Match 4.6%, Score 19, DB 1, Length 19;

Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 EKEDEDEDEPCQAKDEL 417  
DB 1 EKEDEDEDEPCQAKDEL 19

RESULT 2

US-08-045-261-9  
Sequence 9, Application US/08045261  
Patent No. 6426097 *checked*  
GENERAL INFORMATION: *binding of cal. to TC*  
APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOPUT  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-045-261-9

Query Match 4.1%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 SGTIFDNFLITNDEAYA 339  
DB 1 SGTIFDNFLITNDEAYA 17

RESULT 3

US-08-818-253-61  
Sequence 61, Application US/08818253  
Patent No. 5998204  
GENERAL INFORMATION:  
APPLICANT: Tsien, Roger Y.  
APPLICANT: Miyawaki, Atsushi  
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,253  
FILING DATE: 14-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07257/043001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-818-253-61  
Query Match 3.6%; Score 15; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTSPVLGLGLA 15  
DB 1 MLTSPVLGLGLA 15

RESULT 4  
US-08-946-026-53  
Sequence 53, Application US/08946026  
Patent No. 6034218 *no TC caln*  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Dillon, David C.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Mitcham, Jennifer L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/946,026  
FILING DATE: 07-OCT-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.42AC1  
TELECOMMUNICATION INFORMATION:



TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-946-026-53

Query Match 3.4%; Score 14; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 PAVYKQFLDGDG 32  
DB 2 PAVYKQFLDGDG 15

RESULT 5  
US-08-675-816-2  
Sequence 2, Application US/08675816  
Patent No. 6171864  
GENERAL INFORMATION:  
APPLICANT: Coughlan, Sean J.  
APPLICANT: Winfrey, Jr., Ron J.  
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 701 Fifth Ave. Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,816  
FILING DATE: 05-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6171864tenburg, Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 750027.401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206-622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-675-816-2

Query Match 3.1%; Score 13; DB 4; Length 415;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IPDPDKKPEMD 254  
DB 244 IPDPDKKPEMD 256

RESULT 6  
US-08-045-261-2  
Sequence 2, Application US/08045261  
Patent No. 6426097  
GENERAL INFORMATION:

Save as #1 result

APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOPUI

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-2

Query Match 2.9%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.6e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 AVYKQFLDGD 31  
DB 1 AVYKQFLDGD 12

RESULT 7  
US-08-045-261-1  
Sequence 1, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:

APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261

FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28, 678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-1

Query Match 2.6%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VFKEQFLDGD 31  
|||||  
DB 2 VFKEQFLDGD 12

RESULT 8  
US-08-045-261-4  
Sequence 4, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:  
APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28, 678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-4

Query Match 2.6%; Score 11; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VFKEQFLDGD 31  
|||||  
DB 2 VFKEQFLDGD 12

RESULT 9  
US-08-818-253-56  
Sequence 56, Application US/08818253  
Patent No. 5998204  
GENERAL INFORMATION:  
APPLICANT: Tsien, Roger Y.  
APPLICANT: Miyawaki, Atsushi  
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
TITLE OF INVENTION: DETECTION OF ANALYTES  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,253  
FILING DATE: 14-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07257/043001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-818-253-56

Query Match 2.6%; Score 11; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00077;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLLGLLGLA 15  
|||||  
DB 5 VPLLGLLGLA 15

RESULT 10  
US-08-818-252-56  
Sequence 56, Application US/08818252B  
Patent No. 6197928  
GENERAL INFORMATION:  
APPLICANT: Tsien, Roger Y.  
APPLICANT: Miyawaki, Atsushi  
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
TITLE OF INVENTION: DETECTION OF ANALYTES  
FILE REFERENCE: 07257/042001  
CURRENT APPLICATION NUMBER: US/08/818,252B  
CURRENT FILING DATE: 1997-03-14  
NUMBER OF SEQ ID NOS: 56

SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 56  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-08-818-252-56

Query Match 2.6%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00077;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLLGLGLGA 15  
|||||  
DB 5 VPLLGLGLGA 15

RESULT 11  
US-08-675-816-6  
Sequence 6, Application US/08675816  
Patent No. 6171864  
GENERAL INFORMATION:

APPLICANT: Coughlan, Sean J.  
APPLICANT: Winfrey, Jr., Ron J.  
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry  
STREET: 701 Fifth Ave. Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,816  
FILING DATE: 05-JUL-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: No. 6171864tenburg, Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 750027.401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)-622-4900  
TELEFAX: (206)-682-6031

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 542 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-675-816-6

Query Match 2.6%; Score 11; DB 4; Length 542;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 KPEDWDERAKI 225  
|||||  
DB 234 KPEDWDERAKI 244

RESULT 12  
US-08-045-261-3  
Sequence 3, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:  
APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Kelsuke  
APPLICANT: Ryan, Jane

APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOPUI

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-3

Query Match 2.4%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0049;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 YFKEQFLDGD 31  
|||||  
DB 3 YFKEQFLDGD 12

RESULT 13  
US-08-045-261-5  
Sequence 5, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:

APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Kelsuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOPUI  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-5

Query Match 2.4%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0049;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 YKRFQFLDGD 31  
Db 3 YKRFQFLDGD 12

RESULT 14  
US-08-045-261-6  
Sequence 6, Application US/08045261  
Patent No. 5426097  
GENERAL INFORMATION:  
APPLICANT: Stern, David M.  
APPLICANT: Kuwabara, Keisuke  
APPLICANT: Ryan, Jane  
APPLICANT: Benedict, Claude  
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White - Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,261  
FILING DATE: 19930406  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOPUI  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-045-261-6

Query Match 2.4%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0049;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 YKRFQFLDGD 31  
Db 3 YKRFQFLDGD 12

RESULT 15  
US-08-335-198-9  
Sequence 9, Application US/08335198  
Patent No. 5637454  
GENERAL INFORMATION:  
APPLICANT: Harley, John B.  
TITLE OF INVENTION: Assays and Treatments for Autoimmune  
Diseases  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Ste. 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309-4539  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,198  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/648205  
FILING DATE: 01-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF 114CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-335-198-9

Query Match 2.4%; Score 10; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 QIDNPDYKGT 288  
Db 8 QIDNPDYKGT 17

Search completed: March 14, 2003, 20:50:05  
Job time : 25.4986 secs